



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 197923

TO: Ginny Portner
Location: REM/3B02/3C18
Art Unit: 1645
Monday, August 14, 2006
Case Serial Number: 10/780250

From: Vira David
Location: Biotech-Chem Library
REM-1A41
Phone: (571)272-1972

Virajita.David@uspto.gov

Search Notes

Examiner Portner,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Vira David
Intern
STIC Biotech/Chem Library
(571)272-1972

SEQID 1

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STIC-Biotech/ChemLib

197923

From: Portner, Ginny
Sent: Tuesday, August 08, 2006 12:47 PM
To: STIC-Biotech/ChemLib
Subject: 10/780,250

Please search SEQ ID No 1 (polypeptide amino acid sequence). thanks

Ginny Portner
Remsen Building
Art Unit 1645
Room E03, B02; Mail Box 3C18
(571) 272-0862

8/8/2006

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:21:12 ; Search time 44 Seconds
(without alignments)
1607.257 Million cell updates/sec

Title: US-10-780-250-1

Perfect score: 3770
Sequence: 1 EVKQENRLNSESSESSQGL.....TSTNGIKKILIRSKGYENG 735

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3631	96.3	764	2	I39934	protective antigen
2	984	26.1	875	2	I40862	iota toxin compo
3	235.5	6.2	192	2	I39933	cryptic protein -
4	235.5	6.2	204	2	G59104	hypothetical prote
5	209	5.5	468	2	F82885	hypothetical prote
6	203	5.4	1227	2	C97033	uncharacterized pr
7	200	5.3	2529	2	B64635	toxin-like outer m
8	192	5.1	6713	2	B89921	hypothetical prote
9	188	5.0	4919	2	T31105	hypothetical prote
10	187	5.0	1302	1	JC6009	surface-located me
11	186.5	4.9	1072	2	A86827	hypothetical prote
12	183	4.9	4152	2	T31102	filamentous hemag
13	182	4.8	1837	2	T41023	probable nuclear p
14	180	4.8	752	2	G90599	hypothetical prote
15	179.5	4.8	2401	2	T28677	rhoptery protein -
16	179	4.7	2269	2	T28677	rhoptery protein -
17	177	4.7	1553	2	T18502	hypothetical prote
18	177	4.7	3724	2	T18427	hypothetical prote
19	176.5	4.7	2340	2	B71704	cell surface anti
20	175	4.6	1658	2	S55101	hypothetical prote
21	174	4.6	1033	2	T37715	actin-interacting
22	174	4.6	1516	2	E71619	RAD2 endonuclease
23	174	4.6	5005	2	F82884	hypothetical prote
24	172.5	4.6	1024	2	T30868	RhoA-binding prote
25	172	4.6	1939	2	T18372	repeat organellar
26	171.5	4.5	1802	2	S52611	TYB protein - Yeas
27	171.5	4.5	2399	2	H71879	toxin-like outer m
28	170.5	4.5	821	2	S67087	hypothetical prote
29	170.5	4.5	1365	2	T30822	Imp1 protein - Myc

30	170	4.5	2178	2	S55805	alpha-toxin - Clo
31	169.5	4.5	1051	2	T18351	Imp1 protein - Myc
32	169	4.5	1315	2	T28679	fibrinogen-binding
33	169	4.5	1465	2	S31262	TYB protein - Yeas
34	169	4.5	1635	2	A10452	hemolysin [Import
35	169	4.5	1803	2	S56894	TYB protein - Yeas
36	168.5	4.5	979	2	JQ0894	P15 protein - Myc
37	168.5	4.5	1125	2	E90598	membrane nuclease,
38	168	4.5	769	2	F88870	serine proteinase
39	167.5	4.4	1218	2	U80069	hypothetical PI op
40	166.5	4.4	786	2	T18469	hypothetical prote
41	166.5	4.4	2523	2	T18477	hypothetical prote
42	166	4.4	1076	2	C70007	hypothetical prote
43	166	4.4	3216	2	C90538	hypothetical prote
44	165.5	4.4	2526	2	T20531	hypothetical prote
45	165	4.4	1308	2	E71622	probable membrane

ALIGNMENTS

RESULT 1
I39934
protective antigen precursor - Bacillus anthracis plasmid
C:Species: Bacillus anthracis
C:Date: 19-Jul-1996 #sequence revision 19-Jul-1996 #ext_change 09-Jul-2004
C:Accession: I39934; S59160; F59104
R:Velkov, S.U.; Lowe, J.R.; Eden-McClutchan, F.; Vodkin, M.; Leppla, S.H.; Schmidt, J.J.
Gene 69, 287-300, 1988
A:Title: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis
A:Reference number: I39933; PMID:89172073; PMID:3148491
A:Accession: I39934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: protein
A:Residues: 1-764 <RES>
A:Cross-references: UNIPROT:P13423; UNIPARC:UPI0001E609; GB:M22589; NID:G143280; PIDN:f
R:Priddman, T.C.; Gordon, V.M.; Leppla, S.H.; Klimpel, K.R.; Birch, N.P.; Lob, Y.P.
Arch. Biochem. Biophys. 316, 5-13, 1995
A:Title: In vitro processing of anthrax toxin protective antigen by recombinant PC1 (SPC)
A:Reference number: S69160; PMID:95142670; PMID:7840657
A:Accession: S69160
A:Molecule type: protein
A:Residues: 197-202 <FRI>
A:Cross-references: UNIPARC:UPI0000179B0E
R:Okimaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler, J.
J. Bacteriol. 181, 6509-6515, 1999
A:Title: Sequence and organization of pXOI, the large Bacillus anthracis plasmid harboring
A:Reference number: A59091; PMID:99445483; PMID:10515943
A:Accession: F59104
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313, 'Q', 315-764 <OKI>
A:Cross-references: UNIPARC:UPI0000001332; GB:AF065404; NID:G4894216; PIDN:AA23414.1; PJ
A:Experimental source: strain Sterne
A>Note: similar to anthrax toxin moiety, protective antigen, pagA formerly pag, plasmid I
C:Genetics:
A:Gene: pXOI-110
A:Genome: plasmid
C:Function:
Y active components edema factor or lethal factor; the complex is internalized by recept
C:Keyword: exotoxin
F:1-29/Domain: signal sequence #status predicted <Sig>
F:30-196/Domain: propeptide #status predicted <Pro>
F:197-202/Product: protective antigen #status experimental <Mat>

Query Match 96.3%; Score 3631; DB 2; Length 764;
Best Local Similarity 97.0%; Pred. No. 1.5e-174;
Matches 716; Conservative 5; Mismatches 11; Indels 6; Gaps 3;

DB 1 EVKQENRLNSESSESSQGLGYFSDLNFOAMVVTSTTGDLSTPSSLENIPISENQYF 60
30 EVKQENRLNSESSESSQGLGYFSDLNFOAMVVTSTTGDLSTPSSLENIPISENQYF 69

QY 61 OSATWSGFIKYKKSDEYTFATSDAHNTMTWVDQEVINKASNSNKIRLEKGRLOYIKIOY 120
DB 90 QSATWSGFIKYKKSDEYTFATSDAHNTMTWVDQEVINKASNSNKIRLEKGRLOYIKIOY 149
QY 121 QRENPTFEGDLFKLYMTDSQNKKEVSSDNLOLPFLKOKS SNRSRKRSTAGPTYPDBDN 180
DB 150 QRENPTFEGDLFKLYMTDSQNKKEVSSDNLOLPFLKOKS SNRSRKRSTAGPTYPDBDN 209
QY 181 DGIPDSLEVEGYTVDVNKKRTFLSPWISNIHEKKGLTYKKSPEKWSSTADSPYDFEKT 240
DB 210 DGIPDSLEVEGYTVDVNKKRTFLSPWISNIHEKKGLTYKKSPEKWSSTADSPYDFEKT 269
QY 241 GRIDKNVSPPEARHPVLAAYPIVHVDMENIILSKNDQSTONTDSQTRITISKTSRSRAN 300
DB 270 GRIDKNVSPPEARHPVLAAYPIVHVDMENIILSKNDQSTONTDSQTRITISKTSRSR-TH 328
QY 301 TVGVISAGYONGF---TGNITTSAGFSNSNSTVAIDHSLSLAGERTWAETMGLTADT 357
DB 329 TSEVHGNEVHAASFDPDIGSV--SAGFSNSNSTVAIDHSLSLAGERTWAETMGLTADT 386
QY 358 ARLANIRYVNTGTAPINNVLPETTSVLGKQOTLATIKAKENQLSQIILAPNNYPSKNLA 417
DB 387 ARLANIRYVNTGTAPINNVLPETTSVLGKQOTLATIKAKENQLSQIILAPNNYPSKNLA 446
QY 418 PIALNAODPSSPTITMNNYQFLIEKTKQLRLTDQVYGNATNFNGRVRVDTGSNW 477
DB 447 PIALNAODPSSPTITMNNYQFLIEKTKQLRLTDQVYGNATNFNGRVRVDTGSNW 506
QY 478 SEVLPOIOTTARILFNGKDLNVERRIAAVNSPDETTKPDMLKEALKIAFGNEPN 537
DB 507 SEVLPOIOTTARILFNGKDLNVERRIAAVNSPDETTKPDMLKEALKIAFGNEPN 566
QY 538 GNLQYQKODITEFDNFPQOTSQNIKNQLAELANATNITVLDKIKLANAMNILLRDKFPH 597
DB 567 GNLQYQKODITEFDNFPQOTSQNIKNQLAELANATNITVLDKIKLANAMNILLRDKFPH 626
QY 598 YDRNNIAVGADESUYKEAHEVINSTBGLLNIIDKIRKILISGYIVIEDETEGKEVIN 657
DB 627 YDRNNIAVGADESUYKEAHEVINSTBGLLNIIDKIRKILISGYIVIEDETEGKEVIN 686
QY 658 DRYDMLNITSRLRODKTFIDPKKYNCKPLVYISNPNYKVVAVYKENTIIINPSENGDTS 717
DB 687 DRYDMLNITSRLRODKTFIDPKKYNCKPLVYISNPNYKVVAVYKENTIIINPSENGDTS 746
QY 718 TNGIKKILIFSKKGYEIG 735
DB 747 TNGIKKILIFSKKGYEIG 764
RESULT 2
140862
Iota toxin component Ib - Clostridium perfringens
C:Species: Clostridium perfringens
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40862; S42774
R:Perelle, S.; Giber, M.; Boquet, P.; Popoff, M.R.
Infect. Immun. 61, 5147-5156, 1993
A:Title: Characterization of Clostridium perfringens iota-toxin genes and expression in
A:Reference number: I40861; MUID:94041537; PMID:8225592
A:Accession: I40862
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-975 <RES>
A:Cross-references: UNIPROT:Q46221; UNIPARC:UPI000008491; EMBL:X73562; NID:g929031; PID

QY 60 FQSAIWGFIKYKKSDEYTFATSDAHNTMTWVDQEVINKASNSNKIRLEKGRLOYIKIOY 119
DB 95 IKSTIRWGRILIPSEDGEYIILSTR-NDVLMQINAKGLIAK---TLKNNMKGOAYNIRIE 150
QY 120 YQREN-----PTEKGLDFKLYMTDSQNKKEVSSDNLOLPFLKOKS SNRSRKRSTAGPTYPDBDN 170
DB 151 IQDNKLSIDNLSVP-----KLYW-ELNKKTVIPEBNLFYDYSKIDEND----- 195
QY 171 AGPTVP-----DRNDGIPDSLEVEGYTVDVNKKRTFLSPWISNIH 211
DB 196 --PPIPNNPFEDVAFPSAWEDEDLDTDNNDIPDAYENKNGTII---KDSIAVKNDSFA 249
QY 212 EKKGLTYKKSPEKWSSTADSPYDFEKTGRIDKNVSPPEARHPVLAAYPIVHVDMENIIL 271
DB 250 E-QGYKTVSYLSISNTAGDPYTDYQKASGSDIAIKLEARDPLVLAAYPVGVGKREKILIT 308
QY 272 SKNDQSTONTDSQTRITISKTSRSR-DANTVGVISAGYONGFTGNITTSAGFSNSNS 330
DB 309 STNEHASS---DGKTVSRATNSKTDANTVGVISAGYONGFTGNITTSYSHTTDNST 364
QY 331 TVALDHSLSAGERTWAETMGLTADTARLANIRYVNTGTAPINNVLPETTSVLGKQOT 390
DB 365 AVODSN---GE-SWNTGLSINKGESAYIANAVRYNTGTAPINNVLPETTLVL-DEET 417
QY 391 LATIKAKENQLSQIILAPNNYPSKNLPIALNAODPSSPTITMNNYQFLIEKTKQLRL 450
DB 418 LATIKAKENQLSQIILAPNNYPSKNLPIALNAODPSSPTITMNNYQFLIEKTKQLRL 477
QY 451 DTDQVYGNATNFNGRVRVDTGSNMSSEVLPOIOTTARILFNGKDLNVERRIAAVNP 510
DB 478 ETTQVSNYGVYKKN-SQGOI-ITBGNMSNYSIQSDVSASIIID-TSGQTERRVAAEQ 534
QY 511 SDPLETTKPDMLKEALKIAFGNEPNGNLOY-QKODITE-FDNPQOTSQNIKNQLA 567
DB 535 GNPEDKT-PEITIGEAIKKAFSAATK-NGELLFYNGIPIDESCEVILFEDNNTSEIKEDLK 592
QY 568 ELANATNITVLDKIKLANAMNILLRDKF--HYDR-NNIANVGADESUYKEAHEVINST 624
DB 593 YLDRKIKLYNV---KLEKGMNILLKVPISYFNFDEYNNFP--ASMSNIDTKNOGLQSV 646
QY 625 EGL-----LANIDKIRKILISGY-----IVEIETEGLEKVINDRYDMLNI 665
DB 647 NKLGETKILIPSKKIAKRYKRYVFSYKSDPSTNSITVINKSKQKTDYLVPEKDYKF 706
QY 666 S-----SIRQDKTFIDPKKYNCKPLVYISNPNYKVVAVYKENTIIINPSENGDTSNGI 721
DB 707 SYEFETGKQSSDIETLITSSGVIFLDNLSTELNSPTEILKEPEIKVPSQDEILDAHNK 766
RESULT 3
139933
Cryptic protein - Bacillus anthracis
C:Species: Bacillus anthracis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
R:Welch, S.L.; Lowe, J.R.; Eder-McCuehan, F.; Vodkin, M.; Leppla, S.H.; Schmidt, J.J.
Gene 69, 287-300, 1986
A:Title: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis
A:Reference number: I39933; MUID:89172073; PMID:3148491
A:Accession: I39933
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-192 <RES>
A:Cross-references: UNIPROT:P13422; UNIPARC:UPI0000168608; GB:M22589; NID:g143280; PIDN:

Query Match 26.1%; Score 984; DB 2; Length 875;
Best Local Similarity 34.2%; Pred. No. 8.6e-42;
Matches 275; Conservative 125; Mismatches 268; Indels 136; Gaps 32;
Rb 35 DTNQKEEITNENTLSSNGLMGYTFADHFKDLTMAPIRKNGDLKFEKKVVDKLLTENDNS 94

Query Match 6.2%; Score 235.5; DB 2; Length 192;
Best Local Similarity 34.6%; Pred. No. 3e-05;
Matches 56; Conservative 36; Mismatches 47; Indels 23; Gaps 6;

A:Molecule type: DNA
A:Residues: 1-1227 <XIR>
A:Cross-reference: UNIPROT:O97K41; UNIPARC:UPI00000CA0A1; GB:AE001437; PIDN:AAK79054.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1080

Query Match 5.4%; Score 203; DB 2; Length 1227;
Best Local Similarity 19.5%; Pred. No. 0.02; Mismatches 285; Indels 280; Gaps 44;
Matches 170; Conservative 139;

```
37 STTGDLSPSELENIPSENOYFOSAIW-SGFIKYKSDERTPATSDNHTMWDQOE 95
14 SATTSAVALSKPAIAYAADNSVSSISNSNEIIVKGE-----VQEBE 58
DB
96 V-INKASNSKIRLEKGRLYQIKYOENPTK-----GLDFKLYWDSQNKKEVI 146
59 VVNNKQNSNS-KVSSSNENQVS--NKNSNPKVSSSSSEIQSINKNVNLOVQNNKSVL 114
147 SSDNLQBELKQKSSNSRKK-----RSTSAQPTVPDRNDGIPDSLEVEGYVDYKPKRT 201
115 AASNVDDEVKQINSNVQTSYIAIGETKVKPDTLITNKALVDARSAAG--TDLSEVEI 172
DB
202 F-----LSPWISNI-----HEKKG-LTKYK 220
173 YDIYSQTAIEAQEAPRNINDGVANVSDYTLGATFVNDANLDSVKKFYFKKATVTKFK 232
DB
221 SSPKWSNLA-----SDPSPDKTGRIDKRVSPAPKPLVAA 258
223 DVATKTSNALKNINNGGERTDYTALEVSQVTPYLDL-----VNKKIVKEQ----- 280
DB
259 YPIVAVDMENIILSKNEPOS-TQNTDSQRTSKSTSTSRDANTVGSISAGYQNGFTGN 317
281 -----NKGRLITTEISDSAASTIAR-INRDLMDMGAVATLEBYQ----- 320
DB
318 ITTSAGFSNSNSTVAIHSLSLAGEKRTAETM-----GLNTADTARLANI-----RYV 367
321 ---AIGANNVPLQHVADVNSLAM--DQRMGDVSEAIIDGINTIMTYINNINSVGTEDEYI 375
DB
368 NTGTAPI-----YVLEPTTSL-VLGNQTLATTAKENQUSQILAPNNY----- 411
376 NSHAVDSNEGNDIDYILNANIIEKTKAGQODL-TIPEVANVKEVYKTLTLDFFYNAAGQT 434
DB
412 ---PSKNLAPLAINADPFSSPTIMANNQPLEKTKQLRLDTQV----- 455
435 TLQDYKAVDPNAQVQDDVAT-----LSDMLKTPDCKTLKALQDKIDISLNSLKXNSG 488
DB
456 YGNIAITYNFENGRVAVDTGSNWSVLPQIOETTARI-IFNGKOLNIVERRIAANVSPDL 514
489 IGNIDYS-----KLQTEAVDASKLBAVNDIDIKKIKADKGRDLTIOELRDSVKKTIYI 542
DB
515 ETT-----KPDMTLKALKIAF-GEFNEPKNLOYGKDIETFPNPDQOTSQNIK----- 563
543 NSTSNVSGKDGSDSYITIGIDGVTETI-NIEFVERIKESGITI---TIEIKKVIIBRI 597
DB
564 NQIARLAIN--ATNIATYLD-----KIKLANAKOMILLRDKKFFHVR--N 601
588 VQLSEVYRIYTGVTVDYKTLGINNNVANDNNIYINAEKAKKQVAKIODIOTRVDNTIN 657
DB
602 NI-----AVGADESIV-----VKEAREVINSSTEGLLNIDKDIRKLSGYIVEIDBT 649
DB
658 NIDVINKIGAGGAVLSDYFNIGITDYOQILDYVNADLKIQNYKOVDDIIEKVEAKISYS 717
DB
650 EGLK-----EVNDRYDMNLNSSLQDGKTFIDFKKNDKLPY-----ISNPKY----- 695
718 BALMRKINIGEAVTDDFKALGLTDI-----NDGLLLYATTDLONNKRYKTADEV 764
DB
696 -----VNVY-AVTKENTIINPSENGDSTNGI 721
765 IARVOAQIEIYRALLMOIN--LGAATTADYNTLGI 796
DB
```

RESULT 7

B64635
toxin-like outer membrane protein HP0922 - Helicobacter pylori (strain 26955)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: B64635
R:Tomb, J.F.; White, O.; Kurlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khakhria, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64635
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2529 <TOM>
A:Cross-reference: UNIPROT:O25579; UNIPARC:UPI00000D3038; GB:AE000602; GB:AE000511; NID:

Query Match 5.3%; Score 200; DB 2; Length 2529;
Best Local Similarity 18.3%; Pred. No. 0.082;
Matches 172; Conservative 121; Mismatches 339; Indels 306; Gaps 38;

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41 GDLSPSELENIP--SENOYFOSAIWSGFIKYKSDERTPATSDNHTMWDQOEVI 97
DB
508 GDLSPSELENIP--SENOYFOSAIWSGFIKYKSDERTPATSDNHTMWDQOEVI 97
DB
98 NKASNSKIRLEKGRLYQIKYOENPTKGLDPLKYWTDSONKKEVISDNLQPLK 157
550 NSBOEGLKQAIQQAQOQK-QQKQEQQAQOQYQEBLTHSOSLNDVADN-----TIA 604
DB
158 QKSNRSKRSSTSAQPTVPDRNDGIPDSLEVEGYVDV-INKKTFLSPWISNHEKGL 216
605 SNDNTYNNQNTALKEDAQGLENTNQQLAQEQDLKQLQANSP--TGFSEQAQFN 662
DB
217 TKYSSPEPKWSTADPYSDFEKVTGRIDK--NVSPEARHVLVAVYVAVDMENIILSK 273
663 QAKQEQDEQTLQNEKTEFNSBOERLQKAIANKPSPSPSHAPTPKHAAPTTPPKV 722
DB
274 NEDSTONTDS-----QTRTISK-----NTSTSRDANTVGS 305
723 PPTPTQNPPEASVWSGVYMLQNKTYSNKGIYIDPNLSGSGSGSNTLSTYTNLFERS 782
DB
306 ISAGYONG-----FTGNITTSAGFSNSN 328
783 FSVNIQNTLLIGNNTBSVNSGLWIGHGGFGYITGFSAANIYLTNNFMTGEGVSND 842
DB
329 S-----STVAIDHSL-----SLAGERT 345
843 GGGANITFEKASDNITMDGLYNDAETVTKMLQTGASQHSYATFPALNNISVTNSFSDMT 902
DB
346 W-----AETWGLMTAD-----TARLANAIRVNT--GTAPIYVLEPTTSLV 384
903 WKSFSFAKNIISFNASISGFTNPGSSVISAANATNSLSFINSRLNGAVNR--LOANSLI 961
DB
385 LKQKQTLATI-----KAKENQUSQILAPNNYPS-----KULAPIAL--NAQ 424
962 FNNQAVFNVLVYSGTSMFNAFTQLGNTNFTLSQSLLNFNGDPTTLQNNANITLGNSQ 1021
DB
425 DDFSPPTIMANNQPLEKTKQLRLDQYGNIAITYNFENGRVAVDTGSNWSVLPQI 484
1022 AAFKNS-LTLLNNSLSDNOSVLANANTSAFNNOQASINTNGS----- 1064
DB
485 QETTARIIENKQDNLV-VERRIAANVSPDLPTTTPDMLKALKIAGFNPENGLQY 543
1065 QATFNSLFFNGGTSLNASSKLANSMSFSNNTT---INLDSVLSASNTSLSANINIFQ 1121
DB
544 GKDIYTF-----DENPDQOTSQNIKQLA----- 567
1122 GASQADFGGNTIITDPAFNPDSASLSLNNLTANQALNFGYTPSLTKALMSVSGQFVIG 1181
DB
568 ---ELNATNYTVLDKIKLANAKOMILLRDKF-----HYDRN 601
1182 NNGDINISDI-NIFDNITKSVTYNILNAQKITGISGANGYEKILFYGMKIOMATYSNN 1240
DB
```


QY 602 NTAAGA-----DESVYKKAHR-----EYIN--SSTEGILNIDKDI-----RKILSG 641
DB 1241 NQJWSPFNPLNSSQIIOESIKNGDLJTIEVLNPNNSASNTFNIABELNYYQASKNPF 1300
QY 642 YIYEIDTGLKEVINDRDMNLISL-----HODGTFIDFKYNDKPLY---IS 690
DB 1301 YSYDYSDNQA-----GTYLITSNIKLFPPKSGTQQAQETTSFPQPLASLNTYKGS 1355
QY 691 NPNYKVVYAVTKENTIIIN---PSENGDSTNGIKKIL 725
DB 1356 SENLKTLLGLISQNSATLKEMIESNQLDITN-INEVL 1392
RESULT 8
B89921
hypothetical protein ebha [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: B89921
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; WUID:21311952; PMID:11418146
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-6713 <KIR>
A/Cross-references: UNIPROT:Q99U54; UNIPARC:UP1000011021A; GB:BA000018; PID:913701232; F
A/Experimental source: strain N315
C/Genetics:
A/Gene: ebha

Query Match 5.1%; Score 192; DB 2; Length 6713;
Best Local Similarity 20.3%; Pred. No. 0.87;
Matches 170; Conservative 128; Mismatches 297; Indels 244; Gaps 42;
QY 9 LNESESSSOGLLGYPSDLNFOAPMVVTS-----STTGDLSPSELENIPISENQYFOGA 63
DB 2468 VQQAASDAKANIQ-TTHLNNQKODLTSQIEGATVNGNSVKTAKODLDGAMQRLSEA 2526
QY 64 IWSGFIKVKSDY-----TFATSDNHVTMWVDDQEVINKASNSKIRLEKRLYOIKI 118
DB 2527 I-ANNDQTAASENYIDADPTKTAFFNMAIT---QAESYLNKHGHTKDK-----QAVQ 2576
QY 119 QYQRENPTKEGL--DKLYWTSQNKKEVYSSNQLDPE---LKQSSNSRKRTSAGP 173
DB 2577 AIQSVTSTENALNGDNLCCAKTEATGAILNLTQMLTPQKTLAKQOVNAQR----- 2628
QY 174 TVPDRDNGIPDSLEVEGYTVDVNKRTEFLSPWISNIHEK-----KGLTKYKSSPEK 225
DB 2629 -----VSGT-DIKNSATSLNNAAMDOLKALIGHDHTIVAGANTNAPSFK 2672
QY 226 WSTASDPY-----SDFEKVTGRI-----DKQVSEARHPLVAAY 259
DB 2673 QGAYTAYNAAKNIYVSGSPVITNADVTAAATQRVNNAETSLNGTNTLATAKQAADALR 2732
QY 260 PIVHV-DMENIILSKEDSTQNTDSQRTISKRTSND-----ANTVGSISA 308
DB 2733 QMTHLSDAKQSTTQIDATQVTVQVS---VRDNATNLDNANNOLRNSIANDDEVKASQ 2789
QY 309 GY-----QNGFTGATTSAGSPNSNSTVALDHSLSLAGERTWAEWGLN----- 353
DB 2790 PIVDADPTDQNAVNTAVTSAGENIINATSOPTLDPASVTAQAAQVNTNKTALNKAQVLANK 2849
QY 354 ----TADTARL-----NANIRYVNTGTAPIYVNLPTTSLVGNQTLATIKAKENQSLI 405
DB 2850 KQETANINRLSHLNAQKODLNTQVTAAPNI-----STVQVTKAEQLDQAM 2898
QY 406 APNNYTPSKRLAIALNADDFSTPTTNNVNOFLSEKTKQALRLTDQVYGNIAF----- 461

DB 2899 ER-----LNGIQDKQVQSVN---FTDADPEKQ-----TAYNNAVTALEN 2937
QY 462 -YWFENGRVAVDTGSMVSLPOIQE-TTARILFNKDLNVERRI--AAVNSDLEF 516
DB 2938 IINQANG-----TNANQSVBALSTVTTTKQALNG-----DRKYADKNNANQTLSTL 2986
QY 517 -----TKPDMTLKEALKTAFGENBENGILQ--YQGDITEFPDFNF 555
DB 2987 DNLNNAQKAVTGNINQAHTVAEVT--QAIQTAQELNTAMGILKSLNDKDTLGSQNR 3044
QY 556 -----OQTSQNIKNQALNATNITYVLDKIKNAKXNILLRDRFHYDRNNIAV 605
DB 3045 DADPEKKAAYNAEYNAENILNKSSTGVN-----PKQVBAARN-----QVNTTKAL 3092
QY 606 GADSEVYKKAHREVTINSSTEG--LNLNDKDIKILSGTIVEIEDTEGLKEVINDRYDL 663
DB 3093 NGTQNL--EKAKQHNATATIDGSLHTNAQKALQQLVOQSTTVAAEQNSQENOKN----- 3144
QY 664 NISS-----LRO---DQKTFIDFKYNDKPLYISNPNYKVVY--AVTKENTIPSEN 713
DB 3145 NVDAAADKLRQSIADNATTKQONQNTD-----ASFN-KKDAVNNAVTTAQGIIDQTTN 3196

RESULT 9

T31105
hypothetical protein 2 - Haemophilus ducreyi
C/Species: Haemophilus ducreyi
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T31105
R/Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, B.J.
J. Bacteriol. 180, 6013-6022, 1998
A/Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A/Reference number: Z20984; WUID:95030326; PMID:9611662
A/Accession: T31105
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-4919 <NAB>
A/Cross-references: UNIPROT:Q9ZHU0; UNIPARC:UP1000011020B; EMBL:AF057696; NID:93929021; F
C/Genetics:
A/Gene: lspa2

Query Match 5.0%; Score 188; DB 2; Length 4919;
Best Local Similarity 20.5%; Pred. No. 0.87;
Matches 187; Conservative 125; Mismatches 323; Indels 276; Gaps 43;
QY 6 NLLNESESSSOGLLGYPSDLNFOAPMVVTSSTGDL-SIPSELENIPISENQYF---Q 61
DB 154 NNSIKKGNQVLGLGEN-KNIGSQAAKTIPIQVYTDQSKISGGLVGEKADFLIIP 212
QY 62 SAWSGFIKVKSDYTFATFS----- 82
DB 213 NGVTLNGVNTINTDFVASTSEVEPEHIKQLVORQKVIIGQGVATNGLSHEDVAAKI 272
QY 83 -----ADNHVTMWVDDQEVINKASNSKIRLEKRLYOIKI-- 118
DB 273 EQQKVSIEGSKPAKLANVTFAAGNLTYDVNTRD--NNNTNPKKPTDNTKRONIATISG 331
QY 119 -----QYQREN---TEKGL-----DFKLYWTSQNK-----KEV 145
DB 332 EASGMYGNIPIFYTDKAGVNHQGVIFAEDDINILTDGNSRLKLVADYRVVVGKDI 391
QY 146 ISSDNLQELKQKSSNSKRRSTSGAPVPRDNDGIPD-SLEVEGYTVVAKKTEFLS 204
DB 392 ELANNQIHADQOLILNATGHVKLNDGSSVVISNNNIGISALMLTLENATVSAAN---IS 447
QY 205 PWISNIHEKKGLTKYKSSPEKWTASDPYSD-----FEKVTGRI-DKQVSEARHPL 254
DB 448 FRYTNDTKLNLISKVS-----ARAADLOSGLNLDKASVLAHKLTLINSDVSLANQK 501
QY 255 LVAAAPYIVHDMENIILSKEDSTQNTDSQRTISKRTSRTSNDANTVGSISAGYONF 314
DB 502 LSA-----NNLKIKKVRDLNLSNSELNANNLTLNTSN-----NITLKKKSKF 543

QY 315 T-GIITTSAGFSNNSSTVAVIDHSLSLAGEFTALFTMGVLTADPARANINRYVGTAP 373
Db 544 TAGMTLTVN---TNNVTLNNDSELA-ANNLTAVTKAVTLNDBASKLSANKLDLVN--- 594
QY 374 IYNNVLPFTSLVLGKNQTLA-----TIKAKEN---QSLQILAPNNYPPSKLAPIALNAD 426
Db 595 -----TDNVTLNSKSTLSAGELTFKKYKQVTLNNDSELAANN-----ISLNA--- 636
QY 427 FSSPTPTMNTNQLFLELEKT--KQLRL---DTDVYGYNLAITNPNNGKRVDTGSNMSEVL 481
Db 637 --SHNVTLNKKSKLSAKADIKAVNLTLPDTE---LTKNQLDINSTYITNNGTIAGIF 690
QY 482 PQIQTETARII FNGKDLNLYERRI-AAVNPSPDLFTTKPDPMTLKEALKIARGFEPNGNL 540
Db 691 ANI--ITTEKLNNEKALILAEQNLPFTVNGSH--YENKGDIVSDKATVTFSSKNS----- 741
QY 541 QYQGDITTEPDPNFNDOOTSQNIKNQLAEALNATNI-----YVLADIKLNAK----- 586
Db 742 -----DFTNSGSKLVVAQNQL--KAVNNNTTISQGDITLIGNVTLNASTFTNSG 790
QY 587 ----NNILIRDKRFHYDRNNIAVGAD--ESVVK-----EAHREVINS- 622
Db 791 NLTVKTLVDGDIQNFNNKGNLTVGEDLHIKSKTKITNDGKLISIKMLNLSSEADFTNSG 850
QY 623 -----STEGLLNIDKDILKILSGYIVAEIDTDEGKEVINDRYDM---LNIS-- 667
Db 851 TLIGTEALKIATKGNFTNKEKAI--LASNSLIDISVABGKTFNNGTIESGKNLTNTNG 908
QY 668 --LRQDKTFIDFKKVDKLPYLYSN-----PNKKVAVYAVTKENTLIINSENGDSTNG 720
Db 909 AFLNVDATIRSPFVNLITSTGNVSNNGTILSNRLN---ITSANFTNES--NOTWASNG 964
QY 721 IKKILIFSKKG 731
Db 965 LLMNII-AKOG 973
RESULT 10
JC6009
surface-located membrane protein lmp3 precursor - Mycoplasma hominis
C:Species: Mycoplasma hominis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JG6009
R:Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G.
J. Bacteriol. 178, 2775-2784, 1996
A:Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene system
A:Reference number: JG6009; MUID:96213016; PMID:8631664
A:Accession: JG6009
A:Molecule type: DNA
A:Residues: 1-1302 <LAD>
A:Cross-references: UNIPROT:Q49547; UNIPARC:UP100000B0501; EMBL:X95601; NID:g1197335; PIR:JC6009
A:Gene: lmp3
C:Genetics:
A:Genetic code: SGCS
C:Superfamily: surface-located membrane protein lmp3; tetratricopeptide repeat homology
C:Keywords: duplication; membrane protein
F:1-24/Domin: signal sequence #status predicted <SIG>
F:25-102/Product: surface-located membrane protein lmp3 #status predicted <MAT>
F:957-992/Domin: tetratricopeptide repeat homology <TT1>
F:993-1026/Domin: tetratricopeptide repeat homology <TT2>
F:1089-1120/Domin: tetratricopeptide repeat homology <TT3>
F:1154-1190/Domin: tetratricopeptide repeat homology <TT4>
Query Match 5.0%; Score 187; DB 1; Length 1302;
Best Local Similarity 18.7%; Pred. No. 0.14; Indels 178; Gaps 28;
Matches 141; Conservative 139; Mismatches 26;
QY 1 EVKQENRLNLESSESSQQLAGYPSDINLFOAPMVVTSSTGDLSPISSELENIPSENQYF 60
Db 476 QVDBANSIKKQLNALIDKANTLLPGLNDNDSEILVAKKESLNALETTNANKKAVNQNDAISM 535
QY 61 QSAIWSGFIKKKSDETTFATSDNNHTVMWVDDQSVINKASNSKKIRLEKRR--LYQIKI 118
Db 111

Db 536 QSA-----KSLDDKVTYKINQNLTEFNNKDKDAKKELEQTKDIDNFLT 579

Qy 119 QYQRENTPEKGL-----DFKLWTDSONKKEVYSIDSNQLPELKQKSSNSR--KKKS 168

Db 580 DDVKNKNRYATLVKDLTNAKDKKSVYKSSNKEIITAND---ELKQALDYAKAKADGI 635

Qy 169 TSAPTVPDRDNDGIPDSLEVEGYTV---DVKNKRTPELSPWISNHEKKGL---TKYKS 221

Db 636 DEANKSKEQSLSDSITNANQNLNTVSDKDIQKXKTELSQELIGASQELNINPTSMQS 695

Qy 222 SPE---KWSASDPYSDFEYKTVGRIDKNVSPEARHPLVAAPVIVHDMENIILSKNEQ 277

Db 696 AKESLDKATVEITTKCLETFNKK---DKDVK-----FKELEKTRKDIDEPI 736

Qy 278 STQNTDQRTISKQTSRDPANTVGVISAGYQNGFNGITTSAGFSNSNSTVALIDS 337

Db 737 NTMKNINPYSLTISELTSKRDSK-----NSVTNSSNKKDIEETANTELKQA 781

Qy 338 LSLAG-ERTVAETMGLNADPARLNANIRYVNTGAPRYNVLPTSLVAGKQTLATIRA 396

Db 782 LAKANTDKAQADNIAKSTYK---QLNNSISSANTLLAKLTD-----KNTIQQAT 829

Qy 397 ---KENQLSQTILAPNNYPSKMLAPIALNAQ-DPESPTITWNTNQLELEKTKQLRDT 452

Db 830 ELEKEVQKQANQVASNNTASMQSAXSSLDKATVEITTKCLEFNNKQDVFKELEQTRKDI 889

Qy 453 DQYVGNATATNPENGRVRVDTGSKNSSEVLPQIQETTAIIFNGKDLNVERLIAVNPDP 512

Db 890 DEF-----INTNKNTPDYSTLISELTSK-----RDSKNSITNSAN 924

Qy 513 PLEETKPDMLTKALAKLAFGNENPQNGNLQYQCKDTEPDFNDOOTSQNIKNQLAELNAT 572

Db 925 KSDLEFNTATELKQALAKA-----NTDKQQAQ-NLARSTKEQLANSISSAN-- 968

Qy 573 NIYVLDRKILNAKQNTLIRDKRFHYDRNNIAVGAD---ESVYKKAHREVIINSSTEGILL 629

Db 969 ---TLAKLT-----DKDNTIQQAKTELEKEVQKQANQVASNNTASM-- 1007

Qy 630 NIDKDIRKILSGYVEIEDTEGLKEVINDR-YDMLNISLSKODGTFPDKKYNKDLPLX 688

Db 1008 ---QSAXSSLDKATVEIT---TKCLEFNNKQDVKFPELEQTRKDIDEFINTNK----- 1054

Qy 689 ISNPNYKNVYAVT---KENTIINPSENGDST 718

Db 1055 -TNENYSTLISELTSKRDSKNSITNSKNSDIET 1087

RESULT 11

A86827

hypotheical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C/Spectes: Lactococcus lactis subsp. lactis

C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C/Accession: A86827

R/Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

A/Reference number: A86825; MUID:21235186; PMID:11337471

A/Accession: A86827

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1072 <STO>

A/Cross-references: UNIPROT:Q9CF64; UNIPARC:UPI00000D4491; GB:AE005176; PDB:1G12724625; P

A/Experimental source: strain IL1403

C/Genetics:

A:Gene: yqfG

Query Match 4.9%, Score 186.5, DB 2; Length 1072;

Best Local Similarity 20.0%; Pred. No. 0.11;

Matches 163; Conservative 135; Mismatches 353; Indels 165; Gaps 30;

Qy 2 VKQENRLINSESSQGLGYEYFSDNFOAPWVNTSTGDSIPSSLEN----- 52

Db 300 VEQVDVASSSTQDANSASLYPISEASSVTDTNTLNSISLSDSISSSQTENSQSGASSSTA 359

QY 53 ----IPENQYFQSA---IWSGFIKYSDBEYTFATSDAHNVYMWDDQEVINKASNSKI 106
 DB 360 EISYSDNSNSLSLSSNQINSNSNSEKDSQSSSLGSSMSNESEHSSNSININETNNSSSL 419
 QY 107 R-----LEKRLVQIKIYORENPEKGLDFKL-----YWDSONKKEVISDMLQJPELK 157
 DB 420 TALLPSPNPFESNSVDDQTSSEASTNSNSISLSPNISSTSDSEASTNSDPSNAEVA 479
 QY 158 QKSSNSRKRSTSGAPTVPDRNDGI-----PDSLEVEGYTVYKRRFLSPWISNHEK 213
 DB 480 NNSLASVNNSSSSVLASTSTADVLGINQSGSDULTQD--SSEISTSGAFLS--SNQTS 534
 QY 214 KGLTKKSSPEKMTASDPRYSDPEKYTGRLD-KVNSPEARHPVAAPIYVHMENIILS 272
 DB 535 EASYNSSSISLSPNISSTSVLESTSSSPNSFNVAEVANNISLAV-----580
 QY 273 KQEDOSTQNTDQTRTISKV-----TSTRDANTVGVISAGYONGFTGNITTSAGFS 325
 DB 581 NNSSSSVLSTSTADVLGINQSGSDULTQDSEISTSGAFLS-----NOTSSEAS 632
 QY 326 NSNSSTVAIDHSLSLAGERTMAETMGLNTADTARLAN-----IRYVNTGT----- 371
 DB 633 NSWSSINSPSLSLSLSSNSESA-TNQSSNSEATKVDNNSSTHSSNLLSSGSDSDSD 691
 QY 372 --APIYVLEPTTSLVYKQOTLATITAKENQLSQ---ILAPNNTYPSKNLAPIALNAQD 425
 DB 692 SPSDSNL--SSSPNLETQNTTSSKPSSEVNNISENPKVSSNSVOENSTDHMSSTPKS 749
 QY 426 DPSSTPTTNNYNOFLEKTKQRLDTPQYGNLATYN---PENGVRVDTGSMSEVLP 482
 DB 750 SSSPSTSTSSSQKESQSN--LMTTBCINPITFNSSSENSASALIT--SYSNNS 804
 QY 483 QIQTETARLIIF-----NGKDL-----NLVERRIAANVPSDPLETTEKDMTLK-EALK 528
 DB 805 ESEETGCLYISNEAQDNQSEIHSLSPSNSNENNVSSISQSAIILSSKSTTKRSSLS 864
 QY 529 IAFGEFEP-NGNIQYQKQDITEFDPNPDQSTSONIKQALAEATNIIYVLDKI---KAN 584
 DB 865 IINSTSHPNQEDQNSSD-----EYKSNNNVESIILQQLNISNKTMMNSLTQSKLS 916
 QY 585 AKKNILIRKRFHYDNNILAVGDESIVKBAHEVINSSTEGLLNIDQIRKILSGIY 644
 DB 917 VYTLPSKSKVTNEKNENSNVSEKILTPQKN-DESONLQITALDLSFNK----- 968
 QY 645 EIEDTEGLKEVIN-----DRYDMLNISLARQ-GKTFIDKATNDKLEIYISNPYK 695
 DB 969 EYETMEDSTKVPKULDNENGRSQNNKSTIAKDKNKVFPKRSFNSKIL----- 1019
 QY 696 VNVYAVTKENTIIINPSNGDTSTNGIKLIFPSKKG 731
 DB 1020 -----DSDNNILKKTIVLKKHG 1036
 RESULT 12
 T31102
 filamentous hemagglutinin 1 - Haemophilus ducreyi
 C:Species: Haemophilus ducreyi
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T31102
 R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
 J. Bacteriol. 180, 6013-6022, 1998
 A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
 A:Reference number: Z20984; PMID:99030326; PMID:9811662
 A:Accession: T31102
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-4152 <WAB>
 A:Cross-references: UNIPROT:Q9ZHU3; UNIPARC:UP100001101PD; EMBL:AF057695; NID:G3929017;
 C:Genetics:
 A:Gene: LepA
 Query Match 4.9%; Score 183; DB 2; Length 4152;

Best Local Similarity 21.4%; Pred. No. 1.2;
 Matches 177; Conservative 129; Mismatches 336; Indels 186; Gaps 43;
 QY 10 NSESSSQGLGYFFSDLPQ-APVAVTSTTGD-----LSIPSELENIIPENQYF 60
 DB 162 SRYESTSQ-LVGKLANILOQKEAKIILNQVGDHESNIQALAEVAGKADLLIYV---- 216
 QY 61 QSAIWSGFIKYSDBEYTFATSDAHNVYMWDDQEVINKASN-----SKIRLEKRLV 114
 DB 217 PNGITLNGKTIINTDFEVVTS-----DIIIPRENGLLSVRKGKVTYIDKQVA 264
 QY 115 QIKIYQ---QRENPEKGLDFKLWYTDSONKKEVISD-----NILQPELKQSS 161
 DB 265 TNGLSHFVAVANNIDQK--KITVAKTENQSVNANITPAAGSLNLIKTRPAPISS 321
 QY 162 NSRKRKSTSGAPTPDRNDGIIPDSLEVEGYTVD---YKRRFLSPWISNHEKGLT 217
 DB 322 GTSR---TSDTPAL-SADAGSWYGSNIKFWVTDKAGVYKHGIIPEENDINIKMGQNA 377
 QY 218 KYKSSPEKKS-----TASDPYSDPEKV---TGRIDKNSPEARHPVAAPIYH 263
 DB 378 SLKEIYAKQDIDLAKDIBLTERGQLQANNKIIINSTGKIN-----LNASEVSADNVN 431
 QY 264 VDMENIILSKNEDOSTQNTDQTRTISKSTSTRDANTVGVSI-----SAGYQNGFTG 316
 DB 432 VASENAL-ENASMSANSIDVYTKIEVRSKVSAGTANIKASNTTLDGSSVVAANKIL 490
 QY 317 NITTSAGFNSN-----SSTVAIDHSLSLAGERTMAETMGLN-----TADTA 358
 DB 491 NYTNATLNGQSLSAKQDELAVNTNHTLNTSSKLSAQANIKTEMLTNGEASVABK 550
 QY 359 KLANIRYVNTGTAPIYVLPPTTSLVYKQOTLATITAKENQLSQIAPNRY-----YRS 413
 DB 551 DINAIDKITNNGQIAGLTANITTKAL--ENRDAALIAHQN-LNFTVNGSHVYNNKGDIVS 607
 QY 414 KQIAPALNAQDPS-----TPITMANYNOFLEKTKQRLDTPQYVGNI---AT 461
 DB 608 KQDAIYTFESNSDFTSNGSKLYDAQNNLTVVANNPFIYTGSEI-----LHGNTVLANK 661
 QY 462 YNFEN-GRVAVDTGSMSEVLQIQTETARLIIFNGKDLNLYER-----RIAAVNP 510
 DB 662 GNFTNSGNLTMKELNISIESPI---NAGNLTGKGLVHSVTVYKQDKLVSIENLNI 718
 QY 511 SPLEETKEDMTL-KEALKIAPG---FNEPNGLYQKQDITEFDPNF-DQOTSQNIKQ 565
 DB 719 SSKTFTNNGTLLGLEALKIAGSGNFTNASGSLA-SNKSLLDIYGNFTNGTIBSVKS- 776
 QY 566 LAELNATNLYTVLDK--ILNNAKNLILDKRFHYDRNNILAVGAD-ESVYKBAHEVINS 622
 DB 777 ---LNTNNYTIINNAVTISYGVNLNTSQG-NFTNDSNGTVMSHDLNITTSQAN--TINK 830
 QY 623 ST-----EGLL-----NIDQIRKILSGYIYEIEDTEGLKEVINDRYDMLNISGL-RQDG 673
 DB 831 NLLAGQGLNLTAKGNITMDSNSTALAVLHNSNDIN-----LNANKYVNIIGETIYQAGN 885
 QY 674 TPIDEFKINDKLPYISNPNYKAVYAVYKENTIIINPSNGDTSTNGI 721
 DB 886 ISVEAKLINDVVL-----SGNITTTTK-----SGNAATVKTINSI 919
 RESULT 13
 T41023
 probable nuclear pore complex-associated protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T41023
 R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z21965
 A:Accession: T41023
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1837 <MUR>

A:Cross-references: UNIPROT:O74424; UNIPARC:UP1000006A0P8; EMBL:AL023860; P1DN:CAA19588.

A:Experimental source: strain 972h-, cosmid cl62

C:Genetics:

A:Gene: SPDB:SPCC162.08c

A:Map position: 3

Query Match 4.8%; Score 182; DB 2; Length 1837;

Best Local Similarity 19.2%; Pred. No. 0.41;

Matches 168; Conservative 155; Mismatches 347; Indels 206; Gaps 39;

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QY 1 EVKQENRLINSESSQGLGYFSDLNFPQAPMVTSTTGDSLSPSELENIPSENOYF 60
DB 773 QLEGSNNHIVMLKSNHLLTST-----VKDKLKADLSMLEKSLSLQODNPHM 819
QY 61 QSAIWSGFIKXKKSDEYTPAT-SADNHTMWDDEVINK-----ASNSNKRLEKG--- 111
DB 820 KAOIES-----SNQETATYDSNMSNRILELSDNRVANSKLSECSDDVRRLTLONSFDL 873
QY 112 RLYQIKIQORENPFPEKGLDPFLYWTDSQNKKEVISDNLQLPBKOKSSNKKRSTSA 171
DB 874 REHQTLVLQLOSNITELKODITLQRT-VRNQLEI-----QTELEKELKFMEEQENIQ 926
QY 172 GPTV-PDRDNDGIPDSLEVEGYTVDV---KMKRFLSPWISNHEKGLTKYKSSPEKMS 227
DB 927 SKLIANKQTTQNPONVEVBALISIELERTKEKLMAALEKSNIQO---KYLASEKTLLE 981
QY 228 TASDYSDF-----EKVTG-----RID-----KNSPEARHPLVAA- 258
DB 982 MNNEHTEQFKHLVSEISITREBEKITSLSRSELDLNRKVEVLKEEKSSSKELAKOLEDAV 1041
QY 259 -----YPIVHYDMENIILSKNED-----OSTQNTDSQRTISKNTSTSR 297
DB 1042 REKOSALSPKQDYKIRSDADRAVITSLEKEDIEKERSLMKEGSHSVESRIVSHGRTOQKR 1101
QY 298 D-----ANTVGSISAGYQ---NGFTG---NITTSa-----GFSNSNS 329
DB 1102 DLRTPEDEVTKYTLKLNKFNBOHSGLSGAEKDMNIQKAKMEDEISLKDVIYLGLENQNK 1161
QY 330 STVAIDHSL-SLAGERTMAETMGANTATLANIRIV-NTGAPPIYNYLPTTSVL- 385
DB 1162 ----LHSHQFDSLSCQIT---VLQONSSENNLISANLEAVQONDRLRELIVSYLRHEKEITMD 1214
QY 386 -----GKNQTLATIKAKENQLSOLILAPNNVYPSKNIAPIALNAQDPFSSTPTM 434
DB 1215 NKVELTIIDNGLNQVKSIGSTYDLSLOELNRLQSLPVSN-----DQTTPTI-I 1263
QY 435 NYNQFLLEI-EKTKQRLDPTDQVYGNIAITYFENGRVAVDTGSSNNSSEVLPOIQETTARI 492
DB 1264 SGSQEVQALLYESNSVLRKQNDKLGKIQELEKEVEKL---NASINPLQTEINELKAEIG 1319
QY 493 FNGKDLNIVE-----RRIAAVNPSPDELTETTKEDMTLKEALKIAPGNEBNGULQOG 544
DB 1320 AKTASILNLMKEVNSRWKLRFOGVLNRYEIVDPTQ---LEELKKNCEALEKKOBELETKL 1375
QY 545 KDITFEDEFNDQOTS-----ONIKQOLAEANA-TNITYVLDIKILAKANMILIRDRKF 596
DB 1376 QETAKETOTFKQVUNSLBEVENVLKKGVQANTKTRILAAANNEKCEMLKSSSL---TRF 1432
QY 597 HYDRNNIIVGADSVVKEAREVINSSTEG-----LLNLIDKDIRKILSGYIVEI--- 646
DB 1433 AHLKQELTNKNKELTSKNAENAMQKEISLQDSNHQLOESASDAEQITKQFQOLKSE 1492
QY 647 -EDTGLKAEVINDRDMANISS--LRQDGKTFID-----FKYNDKPLPIYSNPNYKVN 697
DB 1493 KERTE--KELADSKNELEHLQSEAVDADQKTEISMLEKEIHRLSDKGLVOOVONLSAE 1550
QY 698 VYAVTKENTYIINSENGPTSTNGIKILIFSKGYE 733
DB 1551 LAALREHSTQGSLENADEIAR-LASQLESTQOYTE 1585
```

hypothetical protein MYPU 7030 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Dates: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90599
R:Chamblaud, I.; Hellig, R.; Perria, S.; Barbe, V.; Samson, D.; Gallissou, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2151, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: G90599
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-752 <KUR>
A:Cross-references: UNIPROT:Q98PL9; UNIPARC:UP100000C80F4; GB:AL445566; PID:g14090118; P1
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 7030
A:Genetic code: SGC3

Query Match 4.8%; Score 180; DB 2; Length 752;

Best Local Similarity 19.2%; Pred. No. 0.14;

Matches 159; Conservative 130; Mismatches 268; Indels 272; Gaps 42;

```
QY 41 GDLSPSELENIPSENOYFQSAIWSGFIKYKSDETTF-----ATSADNHTMWD 92
DB 20 GTISGISYGIQLPNBSASL-----VKRANLEMFNKNOSYLNKSIEBLINQMOD 69
QY 93 DQEVNKAASN-----SNKRLEKGR--LYQI---KIQORENPFPEKGLPFLYWTDSQ 140
DB 70 ENKSNISANDFPNKVFQSKTPLENGEKITYSVAGKDIYFOI VNSQTTISKSVKITSK 129
QY 141 NKEVISSDNLQLPBKOKSSN--SRKKRSTSAQTPVDRDND-----GIPDSLEVEGYTV 194
DB 130 ISKQVWMD-----KQRLNDFAKNLKRVNFKSSASBEKQSDIWAQFNNKSLKELIKYL 182
QY 195 DVKN-----KTFLSFWISNHEKK---GLTKYKSSPEKWSIASDPY 233
DB 183 DDKRVKKNISENTBFDVELKTENNAAFVGVGENDIAGTVIAIVKYNKNSER-----Y 235
QY 234 SDFEVYTCRIDKN-----VSPERHPLVAAAPYIVHYDMENIILSKNEOSTQNTDSQTRT 288
DB 236 QNIQKI-QITNNFRFTPSDES-----LMWELSNKVFEBQSKSN- 276
QY 289 ISKNTSTRDANTVGSISAGYONGFTGNITTSAGFSNSNSTVAIDHSLSLAGERTVAE 348
DB 277 -----DA-----SAFSGNSLVSKNSLKN-----DEKIKLBS--VF 307
QY 349 TNGIANTADTARLANIRVNTGTAPYIVNLPITSLVLGKNOQTATIKK-----ENQ 400
DB 308 VFDLKTNNNTKLSYKXRDIK-----FNKLETVESQKGSVGLTYLIGKVVYDGNESIPNR 361
QY 401 LSQILAPNNVYPSKNIAPIALNAQDPFSSTPIIMNYYNQFLELEKTKQRLDPTDQVYGNIA 460
DB 362 LTSLEFRPS---SKESTIILGLKEELSRKCLANSYVDKVELKWTSSKQAITD-KILASTIT 416
QY 461 TYNFE-----NGRVAVDTGSN-----MSEV-LPOIQETTA---RIIFNGKOLNIV 501
DB 417 SKDPQSQANRITIGPAAANDIAKELAKYLTEISVENINQVTLGLYLVKLFKLDKDSFTI 476
QY 502 EERRIAAV-NPSPDELTETTPD-----MTLKEALKIAPGFNEPNGNLQYQGDQITBEPDNF 554
DB 477 NRTITLVLSGPAKYEATKPDDEKMDVEIYKKSLLQIF-----VDDF----- 517
QY 555 DQQTSQNIKNQOLAEANNTIY--TVLDK-----IKNAMKNILIRDR 595
DB 518 -----LNTNLNKNNTTSLSKELRNKRIROSIEDYPIKILNFTNSKEYPWR 563
QY 596 FHYDRNNIIVGADSVVKEAREVINSSTEGLLNLIDKDIRKILSGYIVIEBDETG--LKE 654
DB 564 LDFPDSNEKAI-----EVKNNNDSSSIVNPFKIYKKNK--VHSDKSSGKIED 608
QY 655 VINDRYDMNLNISTLRQDG-KTFIDF-----KKNYDKLP-----LYISNPNYK 695
DB 609 IVFDKVFPSKEVYKNGNAARKFQDFPSFLKQDSQLRQKLPQITTNELKQDISVNDPFLD 668
```

QY 696 VAVYATKEN-----TINPSE--NGDTSTNGIKILLI-----PSK 729
DB 669 ISSNNIRDNPMFEYKRIIEPKDKNAD-DKNGSLKIMVLSLYNNTKFSK 716

RESULT 15

T28676
rhoptry protein - Plasmodium yoelii (fragment)

C:Species: Plasmodium yoelii
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T28676; A45521
R:Stina, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.

Mol. Biochem. Parasitol. 76, 329-332, 1996
A:Title: Comparison of two members of a multigene family coding for high-molecular mass

A:Reference number: Z20507; MUID:97077455; PMID:8920022
A:Accession: T28676

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-2401 <SIN>
A:Cross-references: UNIPROT:Q26226; UNIPARC:UPI000017B647; EMBL:U36927; NID:91041784; PI

Mol. Biochem. Parasitol. 42, 241-246, 1990
R:Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.

A:Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple cd
A:Reference number: A45521; MUID:91101660; PMID:2270106

A:Accession: A45521
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 2260-2401 <KEE>
A:Cross-references: UNIPARC:UPI000017B648; GB:M34281

Query Match 4.8%; Score 179.5; DB 2; Length 2401;
Best Local Similarity 19.2%; Pred. No. 0.81;
Matches 148; Conservative 131; Mismatches 294; Indels 199; Gaps 37;

QY 48 SELENPSENQYQSAIWSGFIKVKKSDEYTFATSADNHTMNVDDQEVINKASNS-----103
DB 352 SHKNETNNKSETIL-DIR-----YIG-----EITNELNKTLEDF 389
QY 104 -NKIRLEKRLVQIKIYOQREN-----TEKGLDFKLYWDSQNKKEVISDNLOPELK 157
DB 390 KKK---EKLSNKKID-EYAKENVQLVVNSNILEIKKHVNDQ-----INIDIKKEKAK 439
QY 158 QKSSNRKRRSTSGAGTPVDRNDGI PDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLT 217
DB 440 QNVYDQKEHMK-----TIP-----PNEWKYQKPSIRIKIM---DEFLSKVKNYNDFD 484
QY 218 K-YKSSPEKMTSDSDYSPDEKTYGRIDKNVSPEARHPVLAAPYIVHVMENII--LSKN 274
DB 485 KYVKEKVE-----SENNKFTLTNRIKTEVSDE---IKKYENKFNDSKSLINETKKS 534
QY 275 EDOSTONTDSQRT-----ISKNTSTSRDANTVGVIS 307
DB 535 IEBEYONINTLKKVDYIKVCLANTNELITNCHNKQTTLDKLANQNIKITIKETMSIDKIYT 594
QY 308 AGYON-----GFTGNITTSAGFSNSNSTVAIDHSLSLA-----GEET 345
DB 595 DKFENILTDKTELETFTFGLSLNHNSNKKELTYFYDLKANVIGKNKENMLYKOFNEKE 654
QY 346 WA-ETWGLTADYAKLANIRYVNTGAPLYNVLPFTSLVLSGN-----QTLATIKAKE 398
DB 655 KAVEDIKKKNVDINKIVSNIET--TIYTSIYNINEDTENEIGKSIELNTKVLKVKVANY 712
QY 399 NOLSOI-----LAPNNYPSKULADIALNAODFSTPTIMNNOFLELEKT 445
DB 713 TNLNEIKKELKADYDPODFGKELIKTFDEN---KIKNDIDTANQKIDKSIETLTETIKKN 768
QY 446 KQRLDLDQYVGNIAATYFENGVRVYDTGSNWSEVLPOIQTETARIIFN-GKDLNLEVR 504
DB 769 SEVHI--DEIKGIDKLK-----KVPNKTMFNEDEPREIKKILENIYEKIDKKKNYKEI 820
QY 505 IAAVNPSPLETTKPMVTLKALKIAGFNEPNGNLQYQKQDITFPDFNDOOTSQNIKN 564

DB 821 DKLINEISKIEN---DKTSLKELK-----NINLSY-GKSLGNL---FLQOIDEKKK 865
QY 565 QLAELNATNIY-TVLDKIR-----LNAKNILLIRDR-FHYDRNNAVGADE-----609
DB 866 AEHTIKAMEAYIDDLNLIKKSQOIEKENNINNDIDMDIHKEKKALNISHDDYKRYHTTS 925
QY 610 -----SVKKAHREVINSSTEGLLNIDKDIRKILSGYVIEPTE-GLKEVINDRYD 661
DB 926 KNHKEKISDIRKNSLKIIOFSEBSYIN--DIKKELEKNVLESQNNNTDINDQYLSKIEN 982
QY 662 MLNISLRQDGYTFIDFKKYNDKLPLYISNPNYKVVAVYATKENTLINPSEN 713
DB 983 IYNILKLNKIKKIDKVKREYTD-----IKNNKKIAELSNSKIIITOLKEN 1030

Search completed: August 11, 2006, 20:26:55
Job time : 51 secs

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SQ Sequence 735 AA;
 Query Match 100.0%; Score 3770; DB 8; Length 735;
 Best Local Similarity 100.0%; Pred. No. 1.5e-226;
 Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EVKQENRLNLSSESSOGILGYFSDLNFOAPMVTTSSTGDLSPSSELENIPEENQYF 60
DB 1 EVKQENRLNLSSESSOGILGYFSDLNFOAPMVTTSSTGDLSPSSELENIPEENQYF 60
QY 61 OSATWSGFIKYKKSDEYFATSADNHVTMWDQEVINKASNSKIRLEKGRLYQIKIY 120
DB 61 OSATWSGFIKYKKSDEYFATSADNHVTMWDQEVINKASNSKIRLEKGRLYQIKIY 120
QY 121 QRENTEKGLDFKLYWTDSONKKEVISSDNLQLPELKQKSSNSRKRSTASGPTVPDRDN 180
DB 121 QRENTEKGLDFKLYWTDSONKKEVISSDNLQLPELKQKSSNSRKRSTASGPTVPDRDN 180
QY 181 DGIPDSLEVEGYTVVKNKRFTLSPWISNIHEKKGLTKYKSSPEKMSSTASDPYSPEKYT 240
DB 181 DGIPDSLEVEGYTVVKNKRFTLSPWISNIHEKKGLTKYKSSPEKMSSTASDPYSPEKYT 240
QY 241 GRIDKNVSPEARHPVAAVPIVHVMENIILSKNEDQSTQNTDSQRTISKNTSTSRDAN 300
DB 241 GRIDKNVSPEARHPVAAVPIVHVMENIILSKNEDQSTQNTDSQRTISKNTSTSRDAN 300
QY 301 TVGVISISAGYONGFTGNTTTSAGSNSNSTVAIDHSISLAGERTWAETMGINTADTARL 360
DB 301 TVGVISISAGYONGFTGNTTTSAGSNSNSTVAIDHSISLAGERTWAETMGINTADTARL 360
QY 361 NANIRYVNTGTAPINVLPTTSLVIGKQOTLATIRAKENQLSQIILAPNNYPSKULAPIA 420
DB 361 NANIRYVNTGTAPINVLPTTSLVIGKQOTLATIRAKENQLSQIILAPNNYPSKULAPIA 420
QY 421 LNAQDFFSTPTIMWYNOFLBELKTKQLRLDQVYGNATYVNFENGRVYVDTGSNMSRV 480
DB 421 LNAQDFFSTPTIMWYNOFLBELKTKQLRLDQVYGNATYVNFENGRVYVDTGSNMSRV 480
QY 481 LPQIOTETARITFNGKDLNVERRIAANVPSDPLETTFKDMTLKALKAFFNEPNQNL 540
DB 481 LPQIOTETARITFNGKDLNVERRIAANVPSDPLETTFKDMTLKALKAFFNEPNQNL 540
QY 541 OYQGGDITBEDPFPQOOTSQNTKQNLAEINATYVLDKIKLANKNMILJDKKPFHYDR 600
DB 541 OYQGGDITBEDPFPQOOTSQNTKQNLAEINATYVLDKIKLANKNMILJDKKPFHYDR 600
QY 601 NNIAVGADESIVKKAHREVINSSTEGLLNIDKDIRKILSGYIVELBDEGLKAVIANDRY 660
DB 601 NNIAVGADESIVKKAHREVINSSTEGLLNIDKDIRKILSGYIVELBDEGLKAVIANDRY 660
QY 661 DMLNITSSLRQDKRTIIDEFKKNDKPLIYISNPYKAVYATKENTIIINPSENGDTSTNG 720
DB 661 DMLNITSSLRQDKRTIIDEFKKNDKPLIYISNPYKAVYATKENTIIINPSENGDTSTNG 720
QY 721 IKKILIPSKKGYEIG 735
DB 721 IKKILIPSKKGYEIG 735
  
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RESULT 2
 AAE18289 standard; protein; 735 AA.
 AAE18289;
 07-MAY-2002 (first entry)
 Bacillus subtilis protective antigen (PA) domain 1+2+3+4.
 Immunogenic reagent; immune response; protective antigen; PA; vaccine;
 Bacillus anthracis infection; antibacterial.
 Bacillus subtilis.

XX Key Location/Qualifiers
 FH Misc-difference 285 /note= "Encoded by GAA"
 FT
 FT
 PN WO200204646-A1.
 PD 17-JAN-2002.
 PF 06-JUL-2001; 2001WO-GB003065.
 PR 08-JUL-2000; 2000GB-00016702.
 PA (MINA) UK SEC FOR DEFENCE.
 PI Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
 PI Flick-Smith HC, Bullifent HU, Tibball RW, Topping AW;
 XX WPI; 2002-171720/22.
 DR N-PsDB; AAD29121.
 XX
 XX New immunogenic reagent having a polypeptide of the full length
 PT Protective Antigen of Bacillus anthracis, useful for treating B.
 PT anthracis infection or in preparing a medicament for the prophylaxis or
 PT treatment of the infection.
 XX
 PS Example 5; Fig 3; 40pp; English.
 XX
 XX The present invention relates to an immunogenic reagent, which produces
 CC an immune response that is protective against Bacillus anthracis. The
 CC reagent comprises one or more polypeptides which together represent up to
 CC three domains of the full length Protective Antigen (PA) of Bacillus
 CC anthracis or variants of these, and at least one of the domains comprises
 CC domain 1 or domain 4 of PA or its variant. The invention is used as a
 CC vaccine. The immunogenic reagent is useful in the preparation of a
 CC medicament for the prophylaxis or treatment of B. anthracis infection.
 CC The present sequence is Bacillus subtilis protective antigen domain
 CC 1+2+3+4
 SQ Sequence 735 AA;
 Query Match 96.4%; Score 3634; DB 5; Length 735;
 Best Local Similarity 97.2%; Pred. No. 4.6e-218;
 Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

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QY 1 EVKQENRLNLSSESSOGILGYFSDLNFOAPMVTTSSTGDLSPSSELENIPEENQYF 60
DB 1 EVKQENRLNLSSESSOGILGYFSDLNFOAPMVTTSSTGDLSPSSELENIPEENQYF 60
QY 61 OSATWSGFIKYKKSDEYFATSADNHVTMWDQEVINKASNSKIRLEKGRLYQIKIY 120
DB 61 OSATWSGFIKYKKSDEYFATSADNHVTMWDQEVINKASNSKIRLEKGRLYQIKIY 120
QY 121 QRENTEKGLDFKLYWTDSONKKEVISSDNLQLPELKQKSSNSRKRSTASGPTVPDRDN 180
DB 121 QRENTEKGLDFKLYWTDSONKKEVISSDNLQLPELKQKSSNSRKRSTASGPTVPDRDN 180
QY 181 DGIPDSLEVEGYTVVKNKRFTLSPWISNIHEKKGLTKYKSSPEKMSSTASDPYSPEKYT 240
DB 181 DGIPDSLEVEGYTVVKNKRFTLSPWISNIHEKKGLTKYKSSPEKMSSTASDPYSPEKYT 240
QY 241 GRIDKNVSPEARHPVAAVPIVHVMENIILSKNEDQSTQNTDSQRTISKNTSTSRDAN 300
DB 241 GRIDKNVSPEARHPVAAVPIVHVMENIILSKNEDQSTQNTDSQRTISKNTSTSRDAN 300
QY 301 TVGVISISAGYONGFTGNTTTSAGSNSNSTVAIDHSISLAGERTWAETMGINTADT 357
DB 301 TVGVISISAGYONGFTGNTTTSAGSNSNSTVAIDHSISLAGERTWAETMGINTADT 357
QY 358 NANIRYVNTGTAPINVLPTTSLVIGKQOTLATIRAKENQLSQIILAPNNYPSKULAPIA 417
DB 358 NANIRYVNTGTAPINVLPTTSLVIGKQOTLATIRAKENQLSQIILAPNNYPSKULAPIA 417
  
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QY 418 PIALNAQDDSSPTITMANNQFLEKTKQLRLDQVGNATYFENGVRVDTGSNW 477
DB 418 PIALNAQDDSSPTITMANNQFLEKTKQLRLDQVGNATYFENGVRVDTGSNW 477
QY 478 SEVLPOIQETTAIIIFNGKDLNVERRIAANVPSDLETTKPMTLKEALKIAFGNEPN 537
DB 478 SEVLPOIQETTAIIIFNGKDLNVERRIAANVPSDLETTKPMTLKEALKIAFGNEPN 537
QY 538 GNLQYQKDIITEFDNFDOQTSQNIKNQLAELNATNIYTVLDKIKLNAAKNIIIRKRFH 597
DB 538 GNLQYQKDIITEFDNFDOQTSQNIKNQLAELNATNIYTVLDKIKLNAAKNIIIRKRFH 597
QY 598 YDRNNIAGADESVYKAEHREVINSSTEGLLNIDDKIRKILSGYIVIEIDTEGLKEVIN 657
DB 598 YDRNNIAGADESVYKAEHREVINSSTEGLLNIDDKIRKILSGYIVIEIDTEGLKEVIN 657
QY 658 DRYDMNIISSLRQDGTFTIDFKKNDKLPYISNPYKVVAVTENTIIINSENGDTS 717
DB 658 DRYDMNIISSLRQDGTFTIDFKKNDKLPYISNPYKVVAVTENTIIINSENGDTS 717
QY 718 TNGIKKILIFSKKGYEIG 735
DB 718 TNGIKKILIFSKKGYEIG 735
RESULT 3
ADL16348 standard; protein; 735 AA.
XX ADL16348;
AC ADL16348;
XX 06-MAY-2004 (first entry)
DT 06-MAY-2004 (first entry)
XX Bacillus anthracis PA protein from pBP105 vector.
DE Bacillus anthracis PA protein from pBP105 vector.
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
KW lethal factor; LF; anthrax; antibacterial.
XX Bacillus anthracis.
OS Bacillus anthracis.
XX US2004028695-A1.
PN US2004028695-A1.
XX 12-FEB-2004.
PD 12-FEB-2004.
XX 28-MAR-2003; 2003US-00402466.
PF 28-MAR-2003; 2003US-00402466.
XX 12-APR-2002; 2002US-0372152P.
PR 12-APR-2002; 2002US-0372152P.
XX (PARK/) PARK S.
PA (GIRI/) GIRI L.
XX ParK S, GirI L,
PI ParK S, GirI L,
XX WPI; 2004-168865/16.
DR N-PSDB; ADL16346.
XX Immunogenic composition for preparing a vaccine against a lethal
PT infection of Bacillus anthracis in an animal, comprises an immunizing
PT amount of a recombinant B. anthracis protective antigen protein and/or
PT lethal factor protein.
XX Disclosure; SEQ ID NO 13; 143pp; English.
PS The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunizing amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition and
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is Bacillus anthracis PA
XX protein from pBP105 vector used in the invention.
XX Sequence 735 AA;
SQ

Query Match 96.4%; Score 3634; DB 8; Length 735;
Best Local Similarity 97.2%; Pred. No. 4, 6e-218;
Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;
QY 1 EYKQENRLINSESSSSQGLAGYFSDNLPQAPMVVTSSTTGDLISIPSELENIIPSENOYF 60
DB 1 EYKQENRLINSESSSSQGLAGYFSDNLPQAPMVVTSSTTGDLISIPSELENIIPSENOYF 60
QY 61 QSAIWSGFIKVKKSDRYTATSADNHVTMVDQEVYINAKSNKRLKRGRLYQIKQY 120
DB 61 QSAIWSGFIKVKKSDRYTATSADNHVTMVDQEVYINAKSNKRLKRGRLYQIKQY 120
QY 121 QRENPTKGLDPLKYTDSQNKKEVSSDNLOPELKOKSSNRKRSTAGPTVDRDN 180
DB 121 QRENPTKGLDPLKYTDSQNKKEVSSDNLOPELKOKSSNRKRSTAGPTVDRDN 180
QY 181 DGIPDSLEVEGYTVDVKNRTFLSPWISNIEKKGLTKYKSSPEKSTASDPYDEKYV 240
DB 181 DGIPDSLEVEGYTVDVKNRTFLSPWISNIEKKGLTKYKSSPEKSTASDPYDEKYV 240
QY 241 GRIDKXVSPKARHPLVAAVPIVHVDMENTIISKNEQSTQNTDSQRTTSKNTSIRDN 300
DB 241 GRIDKXVSPKARHPLVAAVPIVHVDMENTIISKNEQSTQNTDSQRTTSKNTSIRDN 300
QY 301 TGVGYSISAGYQNGF--TGNIITTSAGFSNSNSTVAIDHSLSIAGERTAEFTMTADT 357
DB 301 TGVGYSISAGYQNGF--TGNIITTSAGFSNSNSTVAIDHSLSIAGERTAEFTMTADT 357
QY 358 ARLNANIRVYNTGTAPITVNLPTTSLVLGKQTLATIKAKENQSLILAPNNYPSKNLA 417
DB 358 ARLNANIRVYNTGTAPITVNLPTTSLVLGKQTLATIKAKENQSLILAPNNYPSKNLA 417
QY 418 PIALNAQDDSSPTITMANNQFLEKTKQLRLDQVGNATYFENGVRVDTGSNW 477
DB 418 PIALNAQDDSSPTITMANNQFLEKTKQLRLDQVGNATYFENGVRVDTGSNW 477
QY 478 SEVLPOIQETTAIIIFNGKDLNVERRIAANVPSDLETTKPMTLKEALKIAFGNEPN 537
DB 478 SEVLPOIQETTAIIIFNGKDLNVERRIAANVPSDLETTKPMTLKEALKIAFGNEPN 537
QY 538 GNLQYQKDIITEFDNFDOQTSQNIKNQLAELNATNIYTVLDKIKLNAAKNIIIRKRFH 597
DB 538 GNLQYQKDIITEFDNFDOQTSQNIKNQLAELNATNIYTVLDKIKLNAAKNIIIRKRFH 597
QY 598 YDRNNIAGADESVYKAEHREVINSSTEGLLNIDDKIRKILSGYIVIEIDTEGLKEVIN 657
DB 598 YDRNNIAGADESVYKAEHREVINSSTEGLLNIDDKIRKILSGYIVIEIDTEGLKEVIN 657
QY 658 DRYDMNIISSLRQDGTFTIDFKKNDKLPYISNPYKVVAVTENTIIINSENGDTS 717
DB 658 DRYDMNIISSLRQDGTFTIDFKKNDKLPYISNPYKVVAVTENTIIINSENGDTS 717
QY 718 TNGIKKILIFSKKGYEIG 735
DB 718 TNGIKKILIFSKKGYEIG 735
RESULT 4
ADL16344 standard; protein; 735 AA.
XX ADL16344;
AC ADL16344;
XX 06-MAY-2004 (first entry)
DT 06-MAY-2004 (first entry)
XX Bacillus anthracis wild-type rPA protein #1.
DE Bacillus anthracis wild-type rPA protein #1.
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
KW lethal factor; LF; anthrax; antibacterial.
XX Bacillus anthracis.
OS

PN US2004028695-A1.
 XX 12-FEB-2004.
 PD 28-MAR-2003; 2003US-00402466.
 PP 12-APR-2002; 2002US-0372152P.
 PR (PARK/) PARK S.
 PA (GIRI/) GIRI L.
 PI Park S, Giri L;
 XX MPI: 2004-168865/16.
 DR N-PEDB; ADL16343, ADL16345.
 XX
 PT Immunogenic composition for preparing a vaccine against a lethal
 PT infection of *Bacillus anthracis* in an animal, comprises an immunizing
 PT amount of a recombinant *B. anthracis* protective antigen protein and/or
 PT lethal factor protein.
 XX
 PS Claim 4; SEQ ID NO 9; 143pp; English.
 XX
 CC The present invention relates to immunogenic compositions useful for
 CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in
 CC an animal. The compositions comprise an immunizing amount of a
 CC recombinant *B. anthracis* protective antigen (rPA) protein and a
 CC recombinant *B. anthracis* lethal factor (rLF) protein. The composition and
 CC methods are useful in protecting against anthrax or lethal infections
 CC caused by *B. anthracis*. The present sequence is *Bacillus anthracis* wild-
 CC type rPA protein used in the invention.
 XX
 SQ Sequence 735 AA;

Query Match 96.4%; Score 3634; DB 8; Length 735;
 Best Local Similarity 97.2%; Pred. No. 4,6e-218;
 Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;
 QY 1 EVKQNRRLNBSSESSQGLGTFPSDLNFOAPMVYTSSTGSLSPSSRLNIPSENGYF 60
 DB 1 EVKQNRRLNBSSESSQGLGTFPSDLNFOAPMVYTSSTGSLSPSSRLNIPSENGYF 60
 QY 61 OSATWSGFITKYKKSBEYFATSDAHNVTMVDQEVINKASNSNKLRLKGLYQIKIY 120
 DB 61 OSATWSGFITKYKKSBEYFATSDAHNVTMVDQEVINKASNSNKLRLKGLYQIKIY 120
 QY 121 QRENPTKGLDFKLYWTDSONKKEVYSSDNLQLPELKQKSSNRKRKSTAGPTVPDRN 180
 DB 121 QRENPTKGLDFKLYWTDSONKKEVYSSDNLQLPELKQKSSNRKRKSTAGPTVPDRN 180
 QY 181 DGIPSLVEGTYVAVKRTFLSPWISNIHKKGLTKYKSPKMTASDYSPEKKT 240
 DB 181 DGIPSLVEGTYVAVKRTFLSPWISNIHKKGLTKYKSPKMTASDYSPEKKT 240
 QY 241 GRIDGNVSPKAPVAAPIYVHMENITLSKNEDOSTONTDSOTRTSKTSTSRDN 300
 DB 241 GRIDGNVSPKAPVAAPIYVHMENITLSKNEDOSTONTDSOTRTSKTSTSRDN 300
 QY 301 TVGVISAGYONGF--TGNTTSAGFSNSNSTVAIDHSLSLAGEERTVAETGINTADT 357
 DB 301 TVGVISAGYONGF--TGNTTSAGFSNSNSTVAIDHSLSLAGEERTVAETGINTADT 357
 QY 358 ARLANNITRYVGTAPVIVLFTTSIVLAKNOTLATIRAKENQSLAIPNNYYSKILA 417
 DB 358 ARLANNITRYVGTAPVIVLFTTSIVLAKNOTLATIRAKENQSLAIPNNYYSKILA 417
 QY 418 PIALNAODFSTPTTMYNOFLKLEKTKQLRLDTDOVGNATATNFENGRVRYVTSNW 477
 DB 418 PIALNAODFSTPTTMYNOFLKLEKTKQLRLDTDOVGNATATNFENGRVRYVTSNW 477
 QY 478 SEVLFOIETTARIIFNGKDLNVERRIAANVSPDLFTTKPDMTLKEALKIAFGNEEN 537
 DB 478 SEVLFOIETTARIIFNGKDLNVERRIAANVSPDLFTTKPDMTLKEALKIAFGNEEN 537

QY 538 GNLOYOGKDITEPPNPDOOTSQNIKNQLAELANATNITYVLDPKIKANAKNILLRDKRFH 597
 DB 538 GNLOYOGKDITEPPNPDOOTSQNIKNQLAELANATNITYVLDPKIKANAKNILLRDKRFH 597
 QY 598 YDRNNIAVGADESVYKAEHREVINSSTEGLLINTDKDIRKILSGYIVIEPTDEGLKEVIN 657
 DB 598 YDRNNIAVGADESVYKAEHREVINSSTEGLLINTDKDIRKILSGYIVIEPTDEGLKEVIN 657
 QY 658 DRYDMLNITSIRRODKTPIIDPKYNDKLPYISNPYVAVNTYATVKENTIIINPSNGQTS 717
 DB 658 DRYDMLNITSIRRODKTPIIDPKYNDKLPYISNPYVAVNTYATVKENTIIINPSNGQTS 717
 QY 718 TNGIKKILIFSKGYEIG 735
 DB 718 TNGIKKILIFSKGYEIG 735
 RESULT 5
 ADR40460
 ID ADR40460 standard; protein; 735 AA.
 AC ADR40460;
 DT 18-NOV-2004 (first entry)
 XX
 DE *Bacillus anthracis* protective antigen F313A F314A mutant.
 XX
 XX antibacterial; vaccine; protective antigen; PA; proteolytic degradation;
 XX *B. anthracis* toxin; *B. anthracis* infection; passive immunisation;
 XX inhalation anthrax; cutaneous anthrax; gastrointestinal anthrax; mutant;
 XX murein.
 XX
 XX *Bacillus anthracis*.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 313..314
 FT /note= "Wild type Phe substituted by Ala"
 PN US2004171121-A1.
 PD 02-SEP-2004.
 PP 08-AUG-2003; 2003US-00638006.
 PR 09-AUG-2002; 2002US-0402285P.
 PA (LEBP/) LEBPPLA S H.
 PA (ROSO/) ROSOVITZ M J.
 PA (HSUS/) HSU S D.
 PI Leppia SH, Rosovitz MJ, Hsu SD;
 DR MPI: 2004-625107/60.
 PT Novel *Bacillus anthracis* protective antigen having mutations conferring
 PT enhanced resistance to proteolytic degradation compared to wild type
 PT antigen, useful for inducing antibodies having neutralizing activity
 PT anthrax toxin.
 XX
 PS Claim 11; Page; 30pp; English.
 XX
 CC The invention describes a recombinant *Bacillus anthracis* protective
 CC antigen (PA), modified to incorporate one or more mutations comprising an
 CC amino acid deletion or substitution in a flexible, exposed, or loop
 CC segment of the PA protein, where the one or more mutations confers
 CC enhanced resistance to proteolytic degradation compared to wild type PA.
 CC A pharmaceutical composition (I) comprising PA and physiologically
 CC acceptable carrier or a composition (II) comprising a synthetic construct
 CC encoding PA and a carrier is useful for inducing serum antibodies that
 CC have neutralizing activity for a *B. anthracis* toxin which involves
 CC administering (I) to a mammal (human), sufficient to elicit production of

CC the antibodies. The antibodies protect the mammal against the infection.
 CC (I) is useful for vaccinating a human against B.anthraxis infection. An
 CC anti-PA-antibody containing composition is useful for passively
 CC immunising a mammal against the toxic effect of B.anthraxis. PA is useful
 CC as vaccines to induce serum antibodies which are useful to prevent, treat
 CC or reduced the severity of infections caused by B.anthraxis, such as
 CC inhalation anthrax, cutaneous anthrax and/or gastrointestinal anthrax. PA
 CC exhibits enhanced stability to proteolytic degradation that is increased
 CC by at least 25% compared to proteolytic degradation of wild-type PA under
 CC comparable conditions. This is the amino acid sequence of protective
 CC antigen (PA) F313A F314A mutant. Note: This sequence does not appear in
 CC the specification but has been created by the indexer using information
 CC given in the invention.

XX Sequence 735 AA;

Query Match 96.4%; Score 3634; DB 8; Length 735;

Best Local Similarity 96.8%; Pred. No. 4.6e-218;

Matches 716; Conservative 2; Mismatches 12; Indels 10; Gaps 2;

QY 1 EYKQENRLINSESSSQGLGYFSDLNFOAPVVTSTTGDLSPSSSELENIPSENQYF 60
 DB 1 EYKQENRLINSESSSQGLGYFSDLNFOAPVVTSTTGDLSPSSSELENIPSENQYF 60
 QY 61 OSAINSGPIKVKKSDYTFATSDNHNVTMWVDDQEVYINAKSNKRLKRGRLYOIKIY 120
 DB 61 OSAINSGPIKVKKSDYTFATSDNHNVTMWVDDQEVYINAKSNKRLKRGRLYOIKIY 120
 QY 121 QRENPEFKGLDFGLYTTDSQNKKEVISDNLOPELKQKSSNRKRGSTAGTVPDRDN 180
 DB 121 QRENPEFKGLDFGLYTTDSQNKKEVISDNLOPELKQKSSNRKRGSTAGTVPDRDN 180
 QY 181 DGIPOSLKEVGYTVDVKNKRTFLSPWISNHEKKGLTKYKSPKKSTASDPYDPEKYT 240
 DB 181 DGIPOSLKEVGYTVDVKNKRTFLSPWISNHEKKGLTKYKSPKKSTASDPYDPEKYT 240
 QY 241 GRIDKVSPEARHPVAAVPIYVDMENITLSKREPOSQNTOSTQRTTSKNTSTSRDN 300
 DB 241 GRIDKVSPEARHPVAAVPIYVDMENITLSKREPOSQNTOSTQRTTSKNTSTSRDN 300
 QY 301 T-----VGVISISAGYNGFTGNITTSAGFSNNSSTVAIDHSLSLAGEBTWMTGLNTA 355
 DB 301 SEVHGNAEYHAASADIG-----SVSAGFSNNSSTVAIDHSLSLAGEBTWMTGLNTA 355
 QY 356 DPARLANIRYVNTGTAPYVNLPTTSLVYGKQQTATIKAKENQSLAPNNYPSKX 415
 DB 356 DPARLANIRYVNTGTAPYVNLPTTSLVYGKQQTATIKAKENQSLAPNNYPSKX 415
 QY 416 LAPIALNADDDSSSTPTTMYNNOFLELEKTKQRLDTPDOYGNIAATYFNENGVRVDG 475
 DB 416 LAPIALNADDDSSSTPTTMYNNOFLELEKTKQRLDTPDOYGNIAATYFNENGVRVDG 475
 QY 476 NMSEVLPJOIQTARIIIFNGKDLNVERBPAANVPSDPLETTPDMTLKEALTIARFNE 535
 DB 476 NMSEVLPJOIQTARIIIFNGKDLNVERBPAANVPSDPLETTPDMTLKEALTIARFNE 535
 QY 536 PNGNTLOYQCKDITEFDFNPDQOSTQNIKQQLAELNANTYTVLDKIKLANKNILRDR 595
 DB 536 PNGNTLOYQCKDITEFDFNPDQOSTQNIKQQLAELNANTYTVLDKIKLANKNILRDR 595
 QY 596 FHYDRNNIIVGADSEVYKKAHREVINSSTBGLLANTDKDIRKLSGYIEIETBGLAKY 655
 DB 596 FHYDRNNIIVGADSEVYKKAHREVINSSTBGLLANTDKDIRKLSGYIEIETBGLAKY 655
 QY 656 INDRYDMLNISSLRQDGKTFIDPKKYNDKPLIYISNPYKVNYYATKENTIIINPSENG 715
 DB 656 INDRYDMLNISSLRQDGKTFIDPKKYNDKPLIYISNPYKVNYYATKENTIIINPSENG 715
 QY 716 TSTNGIKLILPCKGYEIG 735
 DB 716 TSTNGIKLILPCKGYEIG 735

RESULT 6

ID ADR40458 standard; protein; 735 AA.

AC ADR40458;

DT 18-NOV-2004 (first entry)

XX Bacillus anthracis wild type protective antigen seqid 2.

XX antibacterial; vaccine; protective antigen; PA; proteolytic degradation;

KW B.anthraxis toxin; B.anthraxis infection; passive immunisation;

XX inhalation anthrax; cutaneous anthrax; gastrointestinal anthrax.

OS Bacillus anthracis.

PN US2004171121-A1.

PD 02-SEP-2004.

XX 08-AUG-2003; 2003US-00638006.

PR 09-AUG-2002; 2002US-0402285P.

PA (LEPP/) LEPPA S H.

PA (ROSO/) ROSOVITZ M J.

XX (HSUS/) HSU S D.

PI Leppla SH, Roseovltz MJ, Hsu SD;

DR WPI, 2004-625107/60.

XX Novel Bacillus anthracis protective antigen having mutations conferring

PT enhanced resistance to proteolytic degradation compared to wild type

PT antigen, useful for inducing antibodies having neutralizing activity

PT anthrax toxin.

PS Example 5; SEQ ID NO 2; 30pp; English.

XX The invention describes a recombinant Bacillus anthracis protective

CC antigen (PA), modified to incorporate one or more mutations comprising an

CC amino acid deletion or substitution in a flexible, exposed, or loop

CC segment of the PA protein, where the one or more mutations confers

CC enhanced resistance to proteolytic degradation compared to wild type PA.

CC A pharmaceutical composition (i) comprising PA and physiologically

CC acceptable carrier or a composition (ii) comprising a synthetic construct

CC encoding PA and a carrier is useful for inducing serum antibodies that

CC have neutralizing activity for a B.anthraxis toxin which involves

CC administering (i) to a mammal (human), sufficient to elicit production of

CC the antibodies. The antibodies protect the mammal against the infection.

CC (I) is useful for vaccinating a human against B.anthraxis infection. An

CC anti-PA-antibody containing composition is useful for passively

CC immunising a mammal against the toxic effect of B.anthraxis. PA is useful

CC as vaccines to induce serum antibodies which are useful to prevent, treat

CC or reduced the severity of infections caused by B.anthraxis, such as

CC inhalation anthrax, cutaneous anthrax and/or gastrointestinal anthrax. PA

CC exhibits enhanced stability to proteolytic degradation that is increased

CC by at least 25% compared to proteolytic degradation of wild-type PA under

CC comparable conditions. This is the amino acid sequence of wild type

CC protective antigen (PA).

XX Sequence 735 AA;

Query Match 96.4%; Score 3634; DB 8; Length 735;

Best Local Similarity 97.2%; Pred. No. 4.6e-218;

Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

QY 1 EYKQENRLINSESSSQGLGYFSDLNFOAPVVTSTTGDLSPSSSELENIPSENQYF 60
 DB 1 EYKQENRLINSESSSQGLGYFSDLNFOAPVVTSTTGDLSPSSSELENIPSENQYF 60
 QY 61 OSAINSGPIKVKKSDYTFATSDNHNVTMWVDDQEVYINAKSNKRLKRGRLYOIKIY 120
 DB 61 OSAINSGPIKVKKSDYTFATSDNHNVTMWVDDQEVYINAKSNKRLKRGRLYOIKIY 120

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Db 61 OSAINSGFIVKXKSDDEYTPATSDAHNVMTWDDQEVINKANSNKRIRLEKGLYQIKIY 120
QY 121 QRENTEKGLDPKLYWTDSONKKEVISSDNLOLPELKOKSSNRKRSTAGPTVPRDN 180
Db 121 QRENTEKGLDPKLYWTDSONKKEVISSDNLOLPELKOKSSNRKRSTAGPTVPRDN 180
QY 181 DGIPLSLVEGYTVVKNKRTPLSPMISNIHEKGLTKYKSSPEKMSSTADSPDFEKT 240
Db 181 DGIPLSLVEGYTVVKNKRTPLSPMISNIHEKGLTKYKSSPEKMSSTADSPDFEKT 240
QY 241 GRIDKNVSPEARHPLVAAYPIVHVMENIISKNEDOSTONTDQTRITSKYTSRDN 300
Db 241 GRIDKNVSPEARHPLVAAYPIVHVMENIISKNEDOSTONTDQTRITSKYTSRDN 300
QY 301 TVGVISAGYGNF--TGNITTSAGFSNSNSTVAIDHSLSLAGERTYAEFTGANTADT 357
Db 301 TSEVGNALVHASFPDIGGSV--SAGFSNSNSTVAIDHSLSLAGERTYAEFTGANTADT 357
QY 358 ARINANIRVYVNGTPIYVNLPTSLVYGNKOTLATITAKENQSLQILAPNNYPSKNLA 417
Db 358 ARINANIRVYVNGTPIYVNLPTSLVYGNKOTLATITAKENQSLQILAPNNYPSKNLA 417
QY 418 PIALNAODFSSTPTMYNQPLELEKTKQLRLDTQVYGNATYTFENGRRVDTGSNW 477
Db 418 PIALNAODFSSTPTMYNQPLELEKTKQLRLDTQVYGNATYTFENGRRVDTGSNW 477
QY 478 SEVLPQIETTARIIIFNGKDLNVERRIAANVPSDPLETTKPDWTKKALKTAFGENEPN 537
Db 478 SEVLPQIETTARIIIFNGKDLNVERRIAANVPSDPLETTKPDWTKKALKTAFGENEPN 537
QY 538 GNLQVQGDITFEDNPOQTSQNKQLAELANATYVVLKIKLANAMNLLIDKRP 597
Db 538 GNLQVQGDITFEDNPOQTSQNKQLAELANATYVVLKIKLANAMNLLIDKRP 597
QY 598 YDRNNIANGADESVYKAEHREYINSTEGLINIDKILKISGYIVLEJDETEGLKEVIN 657
Db 598 YDRNNIANGADESVYKAEHREYINSTEGLINIDKILKISGYIVLEJDETEGLKEVIN 657
QY 658 DRYDMNLNSSLRQDGKTFIDPKKYNKPLYSNPNYKVVAVTKENTINPSENGDTS 717
Db 658 DRYDMNLNSSLRQDGKTFIDPKKYNKPLYSNPNYKVVAVTKENTINPSENGDTS 717
QY 718 TNGIKKILIFSKGYEIG 735
Db 718 TNGIKKILIFSKGYEIG 735

RESULT 7
ADV90293
ID ADV90293 standard, protein, 735 AA.
XX
AC ADV90293;
XX
DT 10-MAR-2005 (first entry)
XX
DE Protease-hydrolysed polypeptide #70.
XX
XX Protease; immune disorder; inflammation; musculoskeletal disease;
XX dermatological disease; gastrointestinal disease; endocrine disease;
XX metabolic disorder; cancer; hematological disease;
XX cardiovascular disease; neurological disease; neurodegenerative disease;
XX growth disorder; respiratory disease; genitourinary disease;
XX gynecological disorder; nutritional disorder; infection; cytostatic;
XX gastroenterical-gen./antiinflammatory; antischmatic; analgesic;
XX antiarthritic; osteopathic; antidiabetic; nephrotropic;
XX cardiovascular-gen.; immunosuppressive; respiratory-gen.; antipeptic;
XX antiallergic; dermatological; enzyme; hydrolysis.
XX
OS Homo sapiens.
XX
PN WO2004113522-A1.
XX
PD 29-DEC-2004.

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XX 18-JUN-2004; 2004WO-BP051173.
PF 18-JUN-2003; 2003EP-00013819.
XX 18-JUN-2003; 2003EP-00013819.
PR 10-NOV-2003; 2003EP-00025851.
XX 10-NOV-2003; 2003EP-00025851.
PR 11-FEB-2004; 2004EP-00003058.
XX 11-FEB-2004; 2004EP-00003058.
XX (DIRE) DIREVO BIOTECH AG.
PI Haupts U, Koltermann A, Scheidig A, Voetemeier C, Ketting U;
DR WPI; 2005-057985/06.
XX
PT Proteases with defined specificity for a target substrate useful for
PT treating a specific disease related to the target substrate, such as
PT cancer, asthma, diabetes, inflammatory disorders and psoriasis.
XX
XX Claim 38; SEQ ID NO 123; 250pp; English.
XX
CC The invention relates to the use of a protease with defined specificity
CC for a target substrate for preparing a medicament for the treatment of a
CC specific disease related to the target substrate. The invention also
CC relates to a pharmaceutical or diagnostic composition comprising one or
CC more enzymes in the use cited, optionally comprising pharmaceutically or
CC diagnostically acceptable carriers, excipients and/or auxiliary agents, a
CC method for cleaving a target substrate in vivo or in vitro comprising
CC contacting the target substrate with a protease as cited in the use
CC mentioned, and a method for treatment of a disease in a patient connected
CC with a specific target substrate comprising administering to the patient
CC a protease with defined specificity for the specific target substrate.
CC The protease hydrolyzes the target substrate and eliminates or reduces
CC one or more biological activities, physico-chemical properties or
CC pharmacological properties of the target protein and/or activates or
CC increases one or more biological activities, physico-chemical properties
CC or pharmacological properties of the target protein, and/or adds one or
CC more biological activities, physico-chemical properties or
CC pharmacological properties to the target protein. The protease may be
CC administered to treat immune disorders, inflammatory disorders,
CC musculoskeletal diseases, dermatological diseases, gastrointestinal
CC diseases, endocrine diseases, metabolic disorder, cancers, hematological
CC diseases, cardiovascular diseases, neurological diseases,
CC neurodegenerative diseases, growth disorders, respiratory diseases,
CC genitourinary diseases, gynecological disorders, nutritional disorders
CC and infections. This sequence represents a polypeptide hydrolysed by a
CC protease used in the scope of the invention.
XX
XX SQ Sequence 735 AA;
XX
XX Query Match 96.4%; Score 3634; DB 9; Length 735;
XX Best Local Similarity 97.2%; Pred. No. 4, 6e-218; Indels 6; Gaps 3;
XX Matches 717; Conservative 4; Mismatches 11;
QY 1 EVKQENRLINSESSSOGILGYFSDLNFOAPMVYTSSTTGDLSPSSLENIPEENGYF 60
Db 1 EVKQENRLINSESSSOGILGYFSDLNFOAPMVYTSSTTGDLSPSSLENIPEENGYF 60
QY 61 OSAINSGFIVKXKSDDEYTPATSDAHNVMTWDDQEVINKANSNKRIRLEKGLYQIKIY 120
Db 61 OSAINSGFIVKXKSDDEYTPATSDAHNVMTWDDQEVINKANSNKRIRLEKGLYQIKIY 120
QY 121 QRENTEKGLDPKLYWTDSONKKEVISSDNLOLPELKOKSSNRKRSTAGPTVPRDN 180
Db 121 QRENTEKGLDPKLYWTDSONKKEVISSDNLOLPELKOKSSNRKRSTAGPTVPRDN 180
QY 181 DGIPLSLVEGYTVVKNKRTPLSPMISNIHEKGLTKYKSSPEKMSSTADSPDFEKT 240
Db 181 DGIPLSLVEGYTVVKNKRTPLSPMISNIHEKGLTKYKSSPEKMSSTADSPDFEKT 240
QY 241 GRIDKNVSPEARHPLVAAYPIVHVMENIISKNEDOSTONTDQTRITSKYTSRDN 300
Db 241 GRIDKNVSPEARHPLVAAYPIVHVMENIISKNEDOSTONTDQTRITSKYTSRDN 300

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Qy	301	IVGVSI\$AGYQNGF---TGNITTSAGFSNSNSTVAIDHSL\$LAGRTVAETMGINTAOT	357
		: :	
Db	300	TSEVHGAEVH\$AFPDIGSV--SAGFSNSNSTVAIDHSL\$LAGRTVAETMGINTAOT	357
Qy	358	ARLNANIRVYNGTAPIYVNVLTPTSLVLCKNOTLATTIKKENOL\$OILLAPNNYPSKILA	417
Db	358	ARLNANIRVYNGTAPIYVNVLTPTSLVLCKNOTLATTIKKENOL\$OILLAPNNYPSKILA	417
Qy	418	PIALNAODDFSTPTITMANYNOFL\$EKTQ\$RLDPTQVYGNATYTFENGRVAVDTGSNW	477
Db	418	PIALNAODDFSTPTITMANYNOFL\$EKTQ\$RLDPTQVYGNATYTFENGRVAVDTGSNW	477
Qy	478	SEVLP\$QI\$OETARIIIFNGKDLNLYERRIAAVNPSPDLETTKQIDMTLKEALKTAFGENBN	537
Db	478	SEVLP\$QI\$OETARIIIFNGKDLNLYERRIAAVNPSPDLETTKQIDMTLKEALKTAFGENBN	537
Qy	538	GNLQY\$GKODITEFDENPDQOTSQNIKNQ\$LAELNATNIYTVL\$DKIKLNAKNQIILIRDRFH	597
Db	538	GNLQY\$GKODITEFDENPDQOTSQNIKNQ\$LAELNATNIYTVL\$DKIKLNAKNQIILIRDRFH	597
Qy	598	YDRNNIAVGAAB\$SVYKEAR\$EVYNST\$EGL\$LNIDQIDKILISGYIV\$EIDT\$GLKEVIN	657
Db	598	YDRNNIAVGAAB\$SVYKEAR\$EVYNST\$EGL\$LNIDQIDKILISGYIV\$EIDT\$GLKEVIN	657
Qy	658	DRYDMLN\$ISL\$Q\$D\$KTFIDFKYNDKLP\$LYISNPNYKVNVA\$VTK\$NTIIN\$P\$ENG\$DTS	717
Db	658	DRYDMLN\$ISL\$Q\$D\$KTFIDFKYNDKLP\$LYISNPNYKVNVA\$VTK\$NTIIN\$P\$ENG\$DTS	717
Qy	718	TNGIKKILIF\$SKGYEIG	735
Db	718	TNGIKKILIF\$SKGYEIG	735

XX	RESULT
XX	1D AEF05331
XX	AEF05331 standard; protein; 735 AA.
XX	AC AEF05331;
XX	DT 23-FEB-2006 (first entry)
XX	DE Recombinant Protective Antigen, rPA, SEQ ID NO:5.
XX	KM protective antigen; PA; antigen; Bacillus anthracis infection;
XX	XX antibacterial; infection.
XX	OS Bacillus anthracis.
XX	PN WO2005123764-A1.
XX	PD 29-DEC-2005.
XX	PF 16-JUN-2005; 2005WO-GB002360.
XX	PR 16-JUN-2004; 2004GB-00013475.
XX	PR 16-JUN-2004; 2004US-0579687P.
XX	PR 15-JUN-2005; 2005US-00153865.
XX	PA (HEAL-) HEALTH PROTECTION AGENCY.
XX	PA (DYNP-) DYNPORT VACCINE CO LLC.
XX	PI Brehm J, Mcenteer I, Vincent P, Allison N, Brehm R, Jack G;
XX	PI Herbert M, Solow BT, Arroyo J, Lapcevic RK;
XX	XX WP1; 2006-067448/07.
XX	DR N-PSDB; AEF05327.
XX	PT New polynucleotide encoding Protective Antigen, useful for inducing an
XX	PT immune response and for protecting against infection by Bacillus
XX	PT anthracis.
XX	PS Claim 4; SEQ ID NO 5; 110pp; English.
XX	

CC The new invention relates to sequences encoding recombinant *Bacillus*
CC anthracis protective antigen (rPA). Specifically described is a nucleic
CC acid sequence (SEQ ID NO: 1), encoding recombinant rPA, or a fragment of
CC the nucleic acid. Also described is an expression vector comprising the
CC new polynucleotide, a host cell comprising the expression vector; a
CC method for producing rPA or its fragment; a polypeptide produced by the
CC method of (3) or which is encoded by the new polynucleotide; a kit
CC comprising one or more of the polynucleotide, expression vector, host
CC cell, or polypeptide; an antigenic composition comprising a polypeptide
CC of (4); and a method of inducing an immune response against infection by
CC *B. anthracis*. The polynucleotide sequence further comprises a
CC polynucleotide encoding a secretion sequence, e.g. ompA, ompF, ompB,
CC pelB, phoA, lamb, beta lactamase, *Staphylococcus aureus* protein A,
CC *Bacillus subtilis* endoglucanase, murine RNase, human growth hormone,
CC enterotoxin ST-II, LT-A or LT-B, or cpg 2 (cpg). The secretion sequence
CC is for periplasmic or extracellular translocation of the expressed
CC polypeptide from a bacterial host cell cytoplasm. The secretion sequence
CC is a cpg 2 (cpg) leader sequence encoded by SEQ ID NO: 3. The polypeptide
CC is useful for manufacturing a medicament for inducing an immune response
CC against infection by *B. anthracis*, and for protecting against infection
CC by *B. anthracis*. The present sequence is recombinant Protective Antigen,
CC rPA, protein sequence.
CC
CC
XX Sequence 735 AA;
90

Query Match	Similarity	96.4%	Score 3634	DB 10	Length 735	
Best Local Match	717	Conservative	4	Mismatches 11	Indels 6	Gaps 3
QY	1	EVKQENRLNLNSESSESSOGGLGYPFDNLFOAPMVYTSSTTGGDLSIPSSLENIPISENOYF	60			
DB	1	EVKQENRLNLNSESSESSOGGLGYPFDNLFOAPMVYTSSTTGGDLSIPSSLENIPISENOYF	60			
QY	61	QSAIWSGFIKTKKSEHYTFATPSADNHNMTMVDQSVINKASNSNKRLEKGLYOIKIOY	120			
DB	61	QSAIWSGFIKTKKSEHYTFATPSADNHNMTMVDQSVINKASNSNKRLEKGRLOYIKIOY	120			
QY	121	QRENPTFEGDLFKLWYTDSONKKEVYSSDNLQLPFLKOKSSNSRKKRSTYSAGPTVDRDN	180			
DB	121	QRENPTFEGDLFKLWYTDSONKKEVYSSDNLQLPFLKOKSSNSRKKRSTYSAGPTVDRDN	180			
QY	181	DGIDPSLEVEGYTVDVNKKRTPLFSLFWISNIHEKKGLTKYKSSPEKWSSTADSPDEKYT	240			
DB	181	DGIDPSLEVEGYTVDVNKKRTPLFSLFWISNIHEKKGLTKYKSSPEKWSSTADSPDEKYT	240			
QY	241	GRIDKNVSPFAHPIVAAVPTVHVMENIILSKNEDOSTQNTDSQRTISKSTSTRDN	300			
DB	241	GRIDKNVSPFAHPIVAAVPTVHVMENIILSKNEDOSTQNTDSQRTISKSTSTRDN	300			
QY	301	TGVGSIASAGYONGF--TGNITTSAGFNSNSSTVAIDHSLSLAGERTWAEITGLTADT	357			
DB	300	TSEVHGNAERHVASPFIDIGSV--SAGFSENSNSSTVAIDHSLSLAGERTWAEITGLTADT	357			
QY	358	ARLANANITVYNTGTPIYNTVLPPTSILVYGRKQTLATIRAKENQLSQIILANNNYPSKQLA	417			
DB	358	ARLANANITVYNTGTPIYNTVLPPTSILVYGRKQTLATIRAKENQLSQIILANNNYPSKQLA	417			
QY	418	PIANAADPFSSPTITMYNNOFLFLEKTKKQLRLDPDQVYGNATATYFENGWRVVDGSNW	477			
DB	418	PIANAADPFSSPTITMYNNOFLFLEKTKKQLRLDPDQVYGNATATYFENGWRVVDGSNW	477			
QY	478	SEVLPQIOETTARILIFNGKIDNLVERRILAAVNSDPLETTKPDWTLKEALKIAFGNEBN	537			
DB	478	SEVLPQIOETTARILIFNGKIDNLVERRILAAVNSDPLETTKPDWTLKEALKIAFGNEBN	537			
QY	538	GNLOYOGKDITFDPNPDOOTSQNIKNQJAEINANITVLDKIKLANAQNILIRKRFH	597			
DB	538	GNLOYOGKDITFDPNPDOOTSQNIKNQJAEINANITVLDKIKLANAQNILIRKRFH	597			
QY	598	YDRNNIAVGADESYYKEAHREYINSTEGLLNLIDKDIRKLISGYIVIEIDTEGLKEVIN	657			
DB	598	YDRNNIAVGADESYYKEAHREYINSTEGLLNLIDKDIRKLISGYIVIEIDTEGLKEVIN	657			

QY 658 DRYDMLNTSLRQDGKTFIDPKKNDKLPYISNPNKYVNVYAATKENTIIINPSENGDTS 717
DB 658 DRYDMLNTSLSLRQDGKTFIDPKKNDKLPYISNPNKYVNVYAATKENTIIINPSENGDTS 717
QY 718 TNGIKKILIFSKKGYEIG 735
DB 718 TNGIKKILIFSKKGYEIG 735
RESULT 9
ID AEF05332 standard; protein; 736 AA.
AC AEF05332;
XX AEF05332;
XX 23-FEB-2006 (first entry)
DE Wild type Protective Antigen, rPA, SEQ ID NO:6.
XX protective antigen; PA; antigen; Bacillus anthracis infection;
KM antibacterial; infection.
XX Bacillus anthracis.
XX WO2005123764-A1.
XX 29-DEC-2005.
XX 16-JUN-2005; 2005WO-GB002360.
XX 16-JUN-2004; 2004GB-00013475.
XX 16-JUN-2004; 2004US-0579687P.
XX 15-JUN-2005; 2005US-00153865.
XX (HEALTH PROTECTION AGENCY.
PA (DYNP-) DYNPOT VACCINE CO LLC.
PI Brehm J, Mcentee I, Vincent P, Allison N, Brehm R, Jack G;
PI Herbert M, Solow BT, Arroyo J, Lapevich RK;
XX WPI; 2006-067448/07.
XX New polynucleotide encoding Protective Antigen, useful for inducing an
PT immune response and for protecting against infection by Bacillus
PT anthracis.
PS Disclosure; SEQ ID NO 6; 110pp; English.
XX The new invention relates to sequences encoding recombinant Bacillus
CC anthracis protective antigen (rPA). Specifically described is a nucleic
CC acid sequence (SEQ ID NO: 1), encoding recombinant rPA; or a fragment of
CC the nucleic acid. Also described is an expression vector comprising the
CC new polynucleotide; a host cell comprising the expression vector; a
CC method for producing rPA or its fragment; a polypeptide produced by the
CC method of (3) or which is encoded by the new polynucleotide; a kit
CC comprising one or more of the polynucleotide, expression vector, host
CC cell, or polypeptide; an antigenic composition comprising a polypeptide
CC of (4); and a method of inducing an immune response against infection by
CC B. anthracis. The polynucleotide sequence further comprises a
CC polynucleotide encoding a secretion sequence, e.g. ompA, ompT, ompF,
CC pelB, phoA, lamB, beta lactamase, Staphylococcus aureus protein A,
CC Bacillus subtilis endoglucanase, murine RNase, human growth hormone,
CC enterotoxin ST-II, LT-A or LT-B, or cpg 2 (cpg). The secretion sequence
CC is for periplasmic or extracellular translocation of the expressed
CC polypeptide from a bacterial host cell cytoplasm. The secretion sequence
CC is a cpg 2 (cpg) leader sequence encoded by SEQ ID NO: 3. The polypeptide
CC is useful for manufacturing a medicament for inducing an immune response
CC against infection by B. anthracis, and for protecting against infection
CC by B. anthracis. The present sequence is the wild type protective
CC Antigen, rPA, protein sequence.
XX Sequence 736 AA;
SQ

Query Match 96.4%; Score 3634; DB 10; Length 736;
Best Local Similarity 97.2%; Pred. No. 4,66-218;
Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;
QY 1 EVKQENRLNSESSESSQGLGYSFSDLNFOAPMVTSTTGDLSIPSELENIPSENOYF 60
DB 2 EVKQENRLNSESSESSQGLGYSFSDLNFOAPMVTSTTGDLSIPSELENIPSENOYF 61
QY 61 OSATWSGFIRYKKKDEYTFATSAADNHYTMVDDQEVINKASNKIRLEKRLQYIKY 120
DB 62 QSAIWSGFIKYKKDEYTFATSAADNHYTMVDDQEVINKASNKIRLEKRLQYIKY 121
QY 121 QRENPTKGLDFKLYMTDSQNKKEVISSDNLQLPELKOKS SNSRKKSTSGAPTPPBDN 180
DB 122 QRENPTKGLDFKLYMTDSQNKKEVISSDNLQLPELKOKS SNSRKKSTSGAPTPPBDN 181
QY 181 DGIPLSLVEGYTVVKNKRTFLSPWISNIHEKGLTKYKSSPERKSTASDPYDFEY 240
DB 182 DGIPLSLVEGYTVVKNKRTFLSPWISNIHEKGLTKYKSSPERKSTASDPYDFEY 241
QY 241 GRIDKNVSPRARHPLVAAPIVHYDMENI ILSKNEDOSTOMTDSOTRTISKNTSRDAN 300
DB 242 GRIDKNVSPRARHPLVAAPIVHYDMENI ILSKNEDOSTOMTDSOTRTISKNTSR-TH 300
QY 301 TVGVISAGYONGF---TGNITTSAGFSNSNSTVAIDHSLSLAGERTWAEIMGINTADT 357
DB 301 TSEVHGNAEYVHASFPIDGSV--SAGFSNSNSTVAIDHSLSLAGERTWAEIMGINTADT 358
QY 358 ARLNANIRYVNTGAPIVNVLPPTSLVLGKQNTLATIKAKENQLSQIIAPNNYPSKULA 417
DB 359 ARLNANIRYVNTGAPIVNVLPPTSLVLGKQNTLATIKAKENQLSQIIAPNNYPSKULA 418
QY 418 PIALNAODFESSSTITMVMYNOFLELEKTKOIRLTDQYGNIAIATVPENGVRVDTGSNW 477
DB 419 PIALNAODFESSSTITMVMYNOFLELEKTKOIRLTDQYGNIAIATVPENGVRVDTGSNW 478
QY 478 SEVLPQIDETARIIIFNGKDLNVERRIAANVPSDPLETTPMDTLKEALKIAGFNEPN 537
DB 479 SEVLPQIDETARIIIFNGKDLNVERRIAANVPSDPLETTPMDTLKEALKIAGFNEPN 538
QY 538 GNLQYQKDIETFPNPDQOTSQNIKNQALAEIANTITVLDKIKLANAKNIIIRDGRFH 597
DB 539 GNLQYQKDIETFPNPDQOTSQNIKNQALAEIANTITVLDKIKLANAKNIIIRDGRFH 598
QY 598 YDRNNIANAGADESVYKHAHEVINSSTEGILLNTDKDIRKILSGIYIEIDTBEGLXEYIN 657
DB 599 YDRNNIANAGADESVYKHAHEVINSSTEGILLNTDKDIRKILSGIYIEIDTBEGLXEYIN 658
QY 658 DRYDMLNTSLRQDGKTFIDPKKNDKLPYISNPNKYVNVYAATKENTIIINPSENGDTS 717
DB 659 DRYDMLNTSLRQDGKTFIDPKKNDKLPYISNPNKYVNVYAATKENTIIINPSENGDTS 718
QY 718 TNGIKKILIFSKKGYEIG 735
DB 719 TNGIKKILIFSKKGYEIG 736
RESULT 10
ID AAE35717 standard; protein; 764 AA.
AC AAE35717;
XX AAE35717;
XX 17-JUN-2003 (first entry)
DE Bacillus anthracis protective antigen.
XX Apoptosis; therapy; inflammatory mediator; intracellular trafficking;
KM infection; prion disease; Alzheimer' disease; hypersecretion disorder;
KM muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease;
KM corticoids; blepharospasm; asthma; protective antigen.
XX Bacillus anthracis.
OS

Query Match	96.4%	Score 3634	DB 6	Length 764
Best Local Similarity	97.2%	Pred. No. 4,9e-218		
Matches 717	Conservative 4	Mismatches 11	Indels 6	Gaps 3
QY 1	EVKQENRLNSESSESSOGCLGYFSEDLNFOAMVYTSSTTGDLSPSSLELNPSSNOYF	60		
DB 30	EVKQENRLNSESSESSOGCLGYFSEDLNFOAMVYTSSTTGDLSPSSLELNPSSNOYF	89		
QY 61	QSAIWSGFIKTKKSDDEYTFATSADNHYTMVVDQEVYINKASNSNKRIRLEKGRLYQIKIY	120		
DB 90	QSAIWSGFIKTKKSDDEYTFATSADNHYTMVVDQEVYINKASNSNKRIRLEKGRLYQIKIY	149		
QY 121	QRENPTXKGLDFKLYMTDSQNKQEVYISSDNLQLPEIKQSSNSRKKRSTSGAFTVDPDRN	180		
DB 150	QRENPTXKGLDFKLYMTDSQNKQEVYISSDNLQLPEIKQSSNSRKKRSTSGAFTVDPDRN	209		
QY 181	DGIPTDLSLEVEGYTUDVKNKRTPLSLSWISNIHKKGLTKTKSSPEKKSTASDPSPDEKXT	240		
DB 210	DGIPTDLSLEVEGYTUDVKNKRTPLSLSWISNIHKKGLTKTKSSPEKKSTASDPSPDEKXT	269		
QY 241	GRIDKNVSPPEARHPLVAAYPIYHVYVMENTILSKNEDOSTQNTDSCRTTISKNTSTSRDAN	300		
DB 270	GRIDKNVSPPEARHPLVAAYPIYHVYVMENTILSKNEDOSTQNTDSCRTTISKNTSTSR-TH	328		
QY 301	TVGVYSISAGYONGF---TGNITTSAGFSNSNSSTVAIDHSLSLAGERIYAAETWGLNTADT	357		
DB 329	TSEVHGNALEVHAASFDPDIGSV--SAGFSNSNSSTVAIDHSLSLAGERIYAAETWGLNTADT	386		
QY 358	ARLANANIVYVGTATPIYVNLPTTSLVGLKNOTLATIRAKENOLSGOILAPNNYPERKNA	417		
DB 387	ARLANANIVYVGTATPIYVNLPTTSLVGLKNOTLATIRAKENOLSGOILAPNNYPERKNA	446		

QY	410	PLAANAODPSSPTITMANNVNOFLBEEKTKOIRLUTDOYVGNIAITYFNENGRVVDTSNM	477
Db	447	PLAANAODPSSPTITMANNVNOFLBEEKTKOIRLUTDOYVGNIAITYFNENGRVVDTSNM	506
QY	478	SEVLPOIQETTRARIIENGKDLNLYERRIAAVNPSDPLETTKEDMTLKBALKIAGFNEPN	537
Db	507	SEVLPOIQETTRARIIENGKDLNLYERRIAAVNPSDPLETTKEDMTLKBALKIAGFNEPN	566
QY	538	GNLQYOGKDITFEDNFDOQTSQNIKNQDLAELATNTIYVLDKIKLAAKNMILIRDRFH	597
Db	567	GNLQYOGKDITFEDNFDOQTSQNIKNQDLAELATNTIYVLDKIKLAAKNMILIRDRFH	626
QY	598	YDRNNIAVAGADESVKAAHREYVNSTEGLNLNIDKDIRKLSGYIEIEDTEGLKEVIN	657
Db	627	YDRNNIAVAGADESVKAAHREYVNSTEGLNLNIDKDIRKLSGYIEIEDTEGLKEVIN	686
QY	658	DRYDMNLISLSLRQDKTFIDPFCKYNDKFLYISNPNKYVNAVYATKENTIIINPBGDTS	717
Db	687	DRYDMNLISLSLRQDKTFIDPFCKYNDKFLYISNPNKYVNAVYATKENTIIINPBGDTS	746
QY	718	TNGIKKILIFSKGYEIG 735	
Db	747	TNGIKKILIFSKGYEIG 764	

RESULT 11

AD195301

ID AD195301 standard; protein; 764 AA.

XX AD195301;

DT 04-NOV-2004 (first entry)

DE B anthracis toxin translocating protein -protective antigen precursor PA.

XX

KW immune response; overlapping synthetic peptide formulation; OSPF;

KW immunostimulant; virucide; antibacterial; antiparasitic; cytoostatic;

KW vaccine; viral; bacterial; parasitic infection; prion disease;

KW neoplastic; toxin translocating protein protective antigen precursor PA.

OS Bacillus anthracis.

XX

PN WC2004002415-A2.

PD 08-JAN-2004.

XX

PF 27-JUN-2003; 2003WO-US020322.

PR 27-JUN-2002; 2002US-0392718P.

XX

PA (DAND) DANA FARBER CANCER INST INC.

XX

PI Ruprecht RW, JIANG S;

DR WPI; 2004-082868/08.

XX

PT Modulating an immune response, useful for treating immune disorders, e.g.,

PT viral, bacterial and parasitic infections, prion diseases, or neoplastic

PT diseases, administering to a subject an overlapping synthetic peptide

PT formulation.

XX

PS Claim 13; SEQ ID NO 209; 175pp; English.

CC

XX The invention relates to a novel method for modulating an immune response

CC comprising administering to a subject an overlapping synthetic peptide

CC formulation (OSPF) which comprises a combination of single chain peptides

CC corresponding to the amino acid sequence of a protein of interest. The

CC method of the invention has immunostimulant, virucide, antibacterial,

CC antiparasitic and cytoostatic applications and may be useful during

CC vaccine production and for treating immune disorders including viral,

CC bacterial and parasitic infections, prion diseases, neoplastic diseases,

CC as well as providing protection against toxins. The current sequence is

CC that of the OSPF-related Bacillus anthracis toxin translocating protein
CC (protective antigen precursor [PA]) of the invention.

XX Sequence 764 AA;

Query Match 96.4%; Score 3634; DB 8; Length 764;

Best Local Similarity 97.2%; Pred. No. 4.9e-218;

Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

```
QY      1 EVKQENRLINSESSSQGLGYYPSDLNFOAPMVVTSSTTGDLSIPSELENIPSENOYF 60
DB      30 EVKQENRLINSESSSQGLGYYPSDLNFOAPMVVTSSTTGDLSIPSELENIPSENOYF 89
QY      61 OSATWSGFIKYKKSDEYTFATSADNHVTMWDDQEVINKASNSNKLRLKGLVQIKIY 120
DB      90 OSATWSGFIKYKKSDEYTFATSADNHVTMWDDQEVINKASNSNKLRLKGLVQIKIY 149
QY     121 QRENPTKGLDFKLWYTSQNKKEVISSDNLQLPELKQSSNSRKRKSTAGPTVPDRDN 180
DB     150 QRENPTKGLDFKLWYTSQNKKEVISSDNLQLPELKQSSNSRKRKSTAGPTVPDRDN 209
QY     181 DGIPLSLEVEGYTVDVKNKRFTFLSPWISNIHEKGLTKYKSSPEKWSASDPYSDPEKVT 240
DB     210 DGIPLSLEVEGYTVDVKNKRFTFLSPWISNIHEKGLTKYKSSPEKWSASDPYSDPEKVT 269
QY     241 GRIDKNVSPKARHPVVAAYPIVHVDMENTILSKNDOSTQNTDSTQRTISKTSTSRDAN 300
DB     270 GRIDKNVSPKARHPVVAAYPIVHVDMENTILSKNDOSTQNTDSTQRTISKTSTSR-TH 328
QY     301 TVGVASISAGYQNGF---TGNITTSAGFNSNSSTVAIDHSLSLAEERTWAEFMGLNTADT 357
DB     329 TSEVHGNAEVAASFDPDIGSV--SAGFNSNSSTVAIDHSLSLAEERTWAEFMGLNTADT 386
QY     358 ARLNANIRYVNTGTAPIYVNLPTTSLVLGKQNTLATIRAKENQLSQIILAPNNYPSKNIL 417
DB     387 ARLNANIRYVNTGTAPIYVNLPTTSLVLGKQNTLATIRAKENQLSQIILAPNNYPSKNIL 446
QY     418 PIALNAQDDFSTPTTMVNOPLLEKTKQRLDLDVQYGNATATNFENGRVRVDTGSNW 477
DB     447 PIALNAQDDFSTPTTMVNOPLLEKTKQRLDLDVQYGNATATNFENGRVRVDTGSNW 506
QY     478 SEVLPFOIETTRARILFNGKDLNVERRIAAVNSPDLFETTKEDMTLKEALKTAFGEFBN 537
DB     507 SEVLPFOIETTRARILFNGKDLNVERRIAAVNSPDLFETTKEDMTLKEALKTAFGEFBN 566
QY     538 GNLQYQSKDITFEFDFNQOTSQNIKNQLABELANITVYLDKIKLNAKMNILIRDKRFH 597
DB     567 GNLQYQSKDITFEFDFNQOTSQNIKNQLABELANITVYLDKIKLNAKMNILIRDKRFH 626
QY     598 YDRNNIANGADSVYKEARREYVINSTGBLLINDKIRKLISGTVIYELBOTEGKLEYIN 657
DB     627 YDRNNIANGADSVYKEARREYVINSTGBLLINDKIRKLISGTVIYELBOTEGKLEYIN 686
QY     658 DRYDMLNLTSSLEQDQKTFIDFKKNDKLPYIISNPNYKVVAVYTKENTIIINSENGDTS 717
DB     687 DRYDMLNLTSSLEQDQKTFIDFKKNDKLPYIISNPNYKVVAVYTKENTIIINSENGDTS 746
QY     718 TNGIKKILIFSKKGYEIG 735
DB     747 TNGIKKILIFSKKGYEIG 764
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RESULT 12

ID ADM29248 standard; protein; 764 AA.

XX AC ADM29248;

XX DT 24-MAR-2005 (first entry)

XX DE B. anthracis protective antigen, PA.

XX KW Protective antigen; bacillus anthracis infection; vaccine; infection;

KW antibacterial.

OS Bacillus anthracis.

XX WO200500884-A1.

XX 06-JAN-2005.

XX 04-JUN-2004; 2004WO-US017736.

XX 05-JUN-2003; 2003US-0476598P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Schneerson R, Lepja S, Robbins JB, Shiloach J, Kubler-Kielb J;

XX Liu D, Majdady F;

XX WPI; 2005-066555/07.

XX N-PEDB; ADM29247.

PT Immunogenic conjugate, useful for inhibiting or treating infection and/or
PT disease caused by Bacillus anthracis or other bacilli, comprises Bacillus
PT capsular poly-gamma-glutamic acid polypeptide covalently linked to
PT carrier.

PS Disclosure; SEQ ID NO 3; 66pp; English.

CC The invention relates to an immunogenic conjugate comprising a Bacillus
CC capsular poly-gamma-glutamic acid (gammaPGA) polypeptide covalently
CC linked to a carrier, where the conjugate elicits an immune response in a
CC subject. Also included are a composition comprising the conjugate and a
CC pharmaceutically acceptable carrier (for use in eliciting an immune
CC response against Bacillus antigenic epitope, preferably Bacillus
CC anthracis antigenic epitope in a subject) and an isolated antibody that
CC binds to the Bacillus capsular gammaPGA polypeptide (that recognizes
CC antigenic epitopes on both the Bacillus capsular gammaPGA polypeptide,
CC or that binds Bacillus anthracis capsular gammaPGA). The carrier may
CC comprise recombinant B. anthracis protective antigen. The composition and
CC conjugate are useful for eliciting an immune response against a Bacillus
CC antigenic epitope in a subject and for inhibiting or treating infection
CC and/or disease caused by B. anthracis or other bacilli. The immune
CC response comprises opsonophagocytic activity. The composition is useful
CC for active immunization for preventing B. anthracis infections and for
CC preparation of immune antibodies. The present sequence represents
CC Bacillus anthracis protective antigen, PA.

XX Sequence 764 AA;

Query Match 96.4%; Score 3634; DB 9; Length 764;

Best Local Similarity 97.2%; Pred. No. 4.9e-218;

Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

```
QY      1 EVKQENRLINSESSSQGLGYYPSDLNFOAPMVVTSSTTGDLSIPSELENIPSENOYF 60
DB      30 EVKQENRLINSESSSQGLGYYPSDLNFOAPMVVTSSTTGDLSIPSELENIPSENOYF 89
QY      61 OSATWSGFIKYKKSDEYTFATSADNHVTMWDDQEVINKASNSNKLRLKGLVQIKIY 120
DB      90 OSATWSGFIKYKKSDEYTFATSADNHVTMWDDQEVINKASNSNKLRLKGLVQIKIY 149
QY     121 QRENPTKGLDFKLWYTSQNKKEVISSDNLQLPELKQSSNSRKRKSTAGPTVPDRDN 180
DB     150 QRENPTKGLDFKLWYTSQNKKEVISSDNLQLPELKQSSNSRKRKSTAGPTVPDRDN 209
QY     181 DGIPLSLEVEGYTVDVKNKRFTFLSPWISNIHEKGLTKYKSSPEKWSASDPYSDPEKVT 240
DB     210 DGIPLSLEVEGYTVDVKNKRFTFLSPWISNIHEKGLTKYKSSPEKWSASDPYSDPEKVT 269
QY     241 GRIDKNVSPKARHPVVAAYPIVHVDMENTILSKNDOSTQNTDSTQRTISKTSTSRDAN 300
DB     270 GRIDKNVSPKARHPVVAAYPIVHVDMENTILSKNDOSTQNTDSTQRTISKTSTSR-TH 328
QY     301 TVGVASISAGYQNGF---TGNITTSAGFNSNSSTVAIDHSLSLAEERTWAEFMGLNTADT 357
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Db      329 TSEVHGHAFAHAFPDIGSV--SAGESSNSSTVAIDHSLAGERTAFETGINTADT 386
QY      358 ARLNANIRYVNTGAPLYNVLPFTSLVAGKQGLIATIKAKENQLSQILAPNNYPSKNLA 417
Db      387 ARLNANIRYVNTGAPLYNVLPFTSLVAGKQGLIATIKAKENQLSQILAPNNYPSKNLA 446
QY      418 PIALNADDPSSPTIMNNVNOGLEETKQLRLDTPQVYNINATYNNENRNVVDGSGN 477
Db      447 PIALNADDPSSPTIMNNVNOGLEETKQLRLDTPQVYNINATYNNENRNVVDGSGN 506
QY      478 SEVLPOIQTETARIIFNGKDLNVERRIAANVPSDPLETTKPMTLKALKAFGEFEPN 537
Db      507 SEVLPOIQTETARIIFNGKDLNVERRIAANVPSDPLETTKPMTLKALKAFGEFEPN 566
QY      538 GNLQYQKDIETEDFPNDOQTSONIKNOALNATNITVYLDKIKLNAXNMLIRDRFH 597
Db      567 GNLQYQKDIETEDFPNDOQTSONIKNOALNATNITVYLDKIKLNAXNMLIRDRFH 626
QY      598 YDRNNINAVGADSEVYKAAHREVNINSSREGLLNIDKDIRKILSGYVEIEDTGLKRVIN 657
Db      627 YDRNNINAVGADSEVYKAAHREVNINSSREGLLNIDKDIRKILSGYVEIEDTGLKRVIN 686
QY      658 DRYDMLNISLRDQKTFIDFKKYNDKPLVYISNPYKVVAVVTKENTINSENGDTS 717
Db      687 DRYDMLNISLRDQKTFIDFKKYNDKPLVYISNPYKVVAVVTKENTINSENGDTS 746
QY      718 TNGIKKILIFSCKGYEIG 735
Db      747 TNGIKKILIFSCKGYEIG 764

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RESULT 13

AED17612

ID AED17612 standard; protein; 764 AA.

AC AED17612;

XX 01-DEC-2005 (first entry)

XX Anthrax toxin protective antigen PrAg.

XX Anthrax toxin; protein engineering; cancer; tumor; neoplasm; cytostatic;
 XX viral infection; virulence; anti-HIV; autoimmune disease; immune disorder;
 XX antitubercular; antitubercular; antidiabetic; muscular-gen.;
 XX immunosuppressive; antiinflammatory; dermatological; antithyroid; anabolic;
 XX immunosuppressive; hypertensive.

XX Bacillus anthracis.

XX Key Location/Qualifiers

XX Peptide 1. 29

XX Protein /label= Signal_peptide

XX /label= Mature_PrAg

XX Cleavage-site 193. 196

XX /note= "Furin cleavage site"

XX WO2005090393-A2.

XX 29-SEP-2005.

XX 09-FEB-2005; 2005WO-US004216.

XX 09-FEB-2004; 2004US-0543417P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Lepria SH, Liu S, Bugge TH;

XX WPI; 2005-649596/66.

XX N-PSDB; AED17611.

XX

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XX

PT Composition comprising a first effector component of a multimeric
 PT bacterial protein toxin, useful for treating cancer including melanoma or
 PT breast cancer, viral infection, or autoimmune disease e.g. rheumatoid
 PT arthritis.
 PS Disclosure; SEQ ID NO 12; 83pp; English.

XX The present invention provides modified bacterial toxins and methods of
 CC using them for targeting specific cell populations. A claimed composition
 CC comprises a first effector component of a multimeric bacterial protein
 CC toxin. The first effector component comprises at least a first monomer
 CC and a different second monomer which form a heterodimer, where the first
 CC and second monomers are each modified by at least 2 of the following
 CC methods: substitution of a native cell-recognition domain for a non-
 CC native cell-recognition domain; substitution of a native proteolytic
 CC activation site for a non-native proteolytic activation site;
 CC modification of the first monomer to generate a first modified monomer,
 CC where the first modified monomer can pair only with the second monomer;
 CC modification of the first monomer and the second monomer, where a second
 CC effector component can bind only at a site formed by the interaction of
 CC the first monomer and the second monomer molecule; or a combination of
 CC these. The first effector component may form a multimeric bacterial
 CC protein toxin component comprising at least 5, 6 or 7 monomers. The
 CC second effector component is selected from anthrax lethal factor (Lpf),
 CC anthrax edema factor, amino acids 1-254 of Lpf or PF59. The bacterial
 CC protein toxin is selected from anthrax toxin, cholera toxin, Shiga toxin,
 CC staphylococcus toxin alpha or pertussis toxin. In an exemplary
 CC embodiment, the invention provides modified anthrax protective antigens
 CC (PrAg) that are dependent on intramolecular complementation for toxicity.
 CC These comprise at least one PrAg monomer in which the native furin
 CC cleavage site is replaced with a cleavage site for matrix
 CC metalloproteinase (MMP) and at least one PrAg monomer in which the native
 CC furin cleavage site is replaced with a cleavage site for a plasminogen
 CC activator. The PrAg monomers are further modified by mutation of the
 CC native LP binding site such that at least 2 modified PrAg monomers are
 CC required to bind LP. These modified PrAg specifically target cells
 CC expressing both MMP and plasminogen activators and have reduced toxicity
 CC relative to unmodified PrAg. The claimed composition is used in a claimed
 CC method of treating a disease. The disease is: cancer, such as a
 CC carcinoma, sarcoma, lymphoma or leukemia, especially melanoma, colon
 CC cancer, breast cancer, bladder cancer, thyroid cancer, liver cancer,
 CC pleural cancer, lung cancer, ovarian cancer, pancreatic cancer, head and
 CC neck cancer, kidney cancer, multiple myeloma, stomach cancer, brain
 CC cancer, Hodgkin's lymphoma or non-Hodgkin's lymphoma, where the cancer
 CC cell expresses at least 2 proteolytic enzymes; a viral infection such as
 CC a human immunodeficiency virus (HIV) infection, a cytomegalovirus
 CC infection, a human papillomavirus infection, a hepatitis B virus
 CC infection, a hepatitis C virus infection, a herpes simplex virus
 CC infection or a herpes varicella zoster virus infection; or an autoimmune
 CC disease, such as rheumatoid arthritis, diabetes mellitus, myasthenia
 CC gravis, systemic lupus erythematosus, Grave's disease, or Addison's
 CC disease. Targeting a cell comprises contacting the cell with the
 CC composition. Preferably, the cell is in a mammal. The cell is killed by
 CC the contacting step. The present sequence is the protein sequence of wild
 CC -type PrAg.

XX Sequence 764 AA;

XX Query Match 96.4%; Score 3634; DB 9; Length 764;

XX Best Local Similarity 97.2%; Pred. No. 4, 9e-218; Indels 6; Gaps 3;

XX Matches 717; Conservative 4; Mismatches 11;

XX 1 EVKQENRLINSESSSSGGLAGYFSDLPNFOAPMVVYTSSTTGDLSPSSLENIENQYF 60

XX 30 EVKQENRLINSESSSSGGLAGYFSDLPNFOAPMVVYTSSTTGDLSPSSLENIENQYF 89

XX 61 QSAIWSGFIKVKKSDBYTPATSDAHNVYTWVDDQVYINAKSNKRLKGLYQIKIY 120

XX 90 QSAIWSGFIKVKKSDBYTPATSDAHNVYTWVDDQVYINAKSNKRLKGLYQIKIY 149

XX 121 QRENPTKGLDPLKLYWTDSONKKEVYSSDNLQPLKQKSSNRKRSSTAGPTVDRDN 180

XX 150 QRENPTKGLDPLKLYWTDSONKKEVYSSDNLQPLKQKSSNRKRSSTAGPTVDRDN 209

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QY 181 DGIPDSLEVEGYTVDVKKRTFLSPWISNIHEKGLTKYKSPPEKSTASDPYDPEKVT 240
Db 210 DGIPELSLEVEGYTVDVKKRTFLSPWISNIHEKGLTKYKSPPEKSTASDPYDPEKVT 269
QY 241 GRIDKNVSPPEARHPVAAVPIVHVMENIILSKNEDOSTQNTDSTRTISKTSTSRDAN 300
Db 270 GRIDKNVSPPEARHPVAAVPIVHVMENIILSKNEDOSTQNTDSTRTISKTSTSR-TH 328
QY 301 TVGYSISAGYONGF--TGNITTSAGFSNSNSTVAIDHSLSLAGERTWAETMGINTADT 357
Db 329 TSEVGNALVHASFDPDIGGSV--SAGFSNSNSSTVAIDHSLSLAGERTWAETMGINTADT 386
QY 358 ARLANIRYVNTGTAPVYVLPPTSLVVGKQNTLATIRAKENQLSQIILAPNNYPSKNILA 417
Db 387 ARLANIRYVNTGTAPVYVLPPTSLVVGKQNTLATIRAKENQLSQIILAPNNYPSKNILA 446
QY 418 PIALNAQDDFSTPTTMYNNOFLIELEKTKQLRLDTDQVYGNATATNFENGRRVDTGSNW 477
Db 447 PIALNAQDDFSTPTTMYNNOFLIELEKTKQLRLDTDQVYGNATATNFENGRRVDTGSNW 506
QY 478 SEVLPQIETTARIIFNGKDLNLVERRIAANVSPDLETTKPDWTLKEALKIAGFNEPN 537
Db 507 SEVLPQIETTARIIFNGKDLNLVERRIAANVSPDLETTKPDWTLKEALKIAGFNEPN 566
QY 538 GNLQVQGDITEPDENPDQOQTSQNKQDLAEINATNTVLDKILNKNMILLIDKXPH 597
Db 567 GNLQVQGDITEPDENPDQOQTSQNKQDLAEINATNTVLDKILNKNMILLIDKXPH 626
QY 598 YDRNNIAVGADESIVYKEAHREVINSSTEGILLINDIKDIRKILSGYIVIEIDTEGLKEYIN 657
Db 627 YDRNNIAVGADESIVYKEAHREVINSSTEGILLINDIKDIRKILSGYIVIEIDTEGLKEYIN 686
QY 658 DRYDMLNTISLRQDQKTFIDFKYNDKLPYISNPNYKVNVTAVTKENTINPSNGDTS 717
Db 687 DRYDMLNTISLRQDQKTFIDFKYNDKLPYISNPNYKVNVTAVTKENTINPSNGDTS 746
QY 718 TNGIKKILIFSKGYEIG 735
Db 747 TNGIKKILIFSKGYEIG 764

```

RESULT 14

AED25934 standard; protein; 764 AA.

```

ID AED25934 standard; protein; 764 AA.
AC AED25934;
DT 01-DEC-2005 (first entry)
XX XX
Db Bacillus anthracis Paga protein.
XX XX
Kw DNA repair; genetic engineering; immune stimulation; immunity;
Kw bacterial infection; infection; antibacterial; Paga; protective antigen.
XX XX
OS Bacillus anthracis.
PN WO2005092372-A2.
PD 06-OCT-2005.
XX XX
PR 02-FEB-2005; 2005MO-US002987.
XX XX
PR 06-FEB-2004; 2004US-00773618.
PR 30-JUN-2004; 2004US-00863599.
PR 30-JUN-2004; 2004US-0584886P.
PR 23-JUL-2004; 2004MO-US023881.
PR 05-AUG-2004; 2004US-05995222P.
XX XX
PA (CERU-) CERUS CORP.
PA (REGC) UNIV CALIFORNIA.
RI Dubensky TW, Portnoy DA, Calendar RL, Cook DN, Hearst JB;

```

XX WPI: 2005-703101/72.
 DR N-PSDB; AED25935.
 XX Novel isolated, asporogenic *Bacillus anthracis* strain being attenuated
 PT for nucleic acid repair and comprising nucleic acid encoding protective
 PT antigen, useful for inducing immune response against *B. anthracis*.
 XX
 PS Disclosure; SEQ ID NO 18; 133pp; English.

XX The invention relates to a modified asporogenic *Bacillus anthracis* strain
 CC (1) that is attenuated for nucleic acid repair e.g. nucleotide excision
 CC repair (NER), where the strain is: (a) defective with respect to at least
 CC one DNA repair enzyme chosen from UvrA, UvrB, UvrC and RecA. (b)
 CC comprising a heterologous expression cassette comprising a nucleic acid
 CC encoding a protective antigen, which is operably linked to an inducible
 CC promoter, (c) a temperature sensitive recA mutant comprising a recA44
 CC comprising a mutation analogous to the V246W mutation of the recA44
 CC allele of *E. coli*, (d) a repressible recA mutant, or (e) defective with
 CC respect to Stage II sporulation protein B (SpoIIb). Also described are:
 CC (1) an isolated, asporogenic *B. anthracis* bacterium that is attenuated
 CC for nucleic acid repair, where the nucleic acid of the *B. anthracis*
 CC bacterium has been modified with a nucleic acid targeting compound that
 CC reacts directly with the nucleic acid so that the bacterium is attenuated
 CC for proliferation; (2) an isolated, sporulation-deficient *B. anthracis*
 CC strain that is attenuated for NER; (3) a *B. anthracis* strain being an
 CC inducible recA mutant or comprising a nucleic acid encoding an antigen,
 CC where the nucleic acid is operably linked to a heterologous promoter; (4)
 CC a vaccine composition comprising any one of the modified *B. anthracis*
 CC strains mentioned above or a bacterium from an asporogenic *B. anthracis*
 CC strain that is attenuated for nucleic acid repair; and (5) the use of the
 CC bacterium from an asporogenic *B. anthracis* strain that is attenuated for
 CC nucleic acid repair in the manufacture of a medicament for inducing an
 CC immune response in a host to *B. anthracis*. The modified *B. anthracis*
 CC strains of the invention are useful for manufacturing a medicament for
 CC inducing an immune response to *B. anthracis* in a host. The vaccine of the
 CC invention is useful for inducing an immune response to *B. anthracis* in a
 CC host. This sequence represents *Bacillus anthracis* protective antigen
 CC (Paga) protein.
 CC
 XX
 SQ Sequence 764 AA;

Query Match 96.4%; Score 3634; DB 9; Length 764;
 Best Local Similarity 97.2%; Pred. No. 4.9e-218;
 Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

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QY 1 EVKQENRLNSESSESSQGLGYPSDLNFOAPMVVTSSTGDLSPSSLENIPISENGYF 60
Db 30 EVKQENRLNSESSESSQGLGYPSDLNFOAPMVVTSSTGDLSPSSLENIPISENGYF 89
QY 61 QSAIWSGFIKYKKSDEYTFATSADNHVTMWDDQEVINKANSNKRIRLEKRLVQIKYQ 120
Db 90 QSAIWSGFIKYKKSDEYTFATSADNHVTMWDDQEVINKANSNKRIRLEKRLVQIKYQ 149
QY 121 QRENPTKGLDPFKLWYTDSONKKEVYISSDNLQPLPKOKSSNSRKGRSTAGPTVPBDN 180
Db 150 QRENPTKGLDPFKLWYTDSONKKEVYISSDNLQPLPKOKSSNSRKGRSTAGPTVPBDN 209
QY 181 DGIPDSLEVEGYTVDVKKRTFLSPWISNIHEKGLTKYKSPPEKSTASDPYDPEKVT 240
Db 210 DGIPELSLEVEGYTVDVKKRTFLSPWISNIHEKGLTKYKSPPEKSTASDPYDPEKVT 269
QY 241 GRIDKNVSPPEARHPVAAVPIVHVMENIILSKNEDOSTQNTDSTRTISKTSTSRDAN 300
Db 270 GRIDKNVSPPEARHPVAAVPIVHVMENIILSKNEDOSTQNTDSTRTISKTSTSR-TH 328
QY 301 TVGYSISAGYONGF--TGNITTSAGFSNSNSTVAIDHSLSLAGERTWAETMGINTADT 357
Db 329 TSEVGNALVHASFDPDIGGSV--SAGFSNSNSSTVAIDHSLSLAGERTWAETMGINTADT 386
QY 358 ARLANIRYVNTGTAPVYVLPPTSLVVGKQNTLATIRAKENQLSQIILAPNNYPSKNILA 417

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Db	367	ALANNAIRVNTGTAIPYVLTPTTSLVGLKNCQTLATITKAKENQSLQILAPNNYTPSKNLA	446
Qy	418	PIANAQDDFSSPTPTMANNQPLELEKTKQLRLDTQVYGNIAATYNFENGRAVVDGSNW	477
Db	447	PIALNAQDDFSSPTPTMANNQPLELEKTKQLRLDTQVYGNIAATYNFENGRAVVDGSNW	506
Qy	418	SEVLVQIQIOTTARIIIFNGKDNLVERRIAANVPSDPLETTKPMTLKALKAFGNREP	537
Db	507	SEVLVQIQIOTTARIIIFNGKDNLVERRIAANVPSDPLETTKPMTLKALKAFGNREP	566
Qy	538	GNLQYQGDQITFEDEFDPQDQTSQNIQNLALNAATNYVTVLDDIKIKNAKKNLILRDRFH	597
Db	567	GNLQYQGDQITFEDEFDPQDQTSQNIQNLALNAATNYVTVLDDIKIKNAKKNLILRDRFH	626
Qy	598	YDRNNIAVGADESYYKEAREVYINSSTEGLLINDIKIRKILSGYIWEIEDTEGLKEVIN	657
Db	627	YDRNNIAVGADESYYKEAREVYINSSTEGLLINDIKIRKILSGYIWEIEDTEGLKEVIN	686
Qy	658	DRYDMNLNTSSLRQDGKTFIDFKKNDKLPYIYSNPNYKKNVYAVTKENTTINSENGDTS	717
Db	687	DRYDMNLNTSSLRQDGKTFIDFKKNDKLPYIYSNPNYKKNVYAVTKENTTINSENGDTS	746
Qy	718	TNGIKKIIILFSKKGYEIG 735	
Db	747	TNGIKKIIILFSKKGYEIG 764	
RESULT 15			
ID	ADR40461	standard, protein, 735 AA.	
XX	ADR40461;		
XX	18-NOV-2004	(first entry)	
DE	Bacillus anthracis	protective antigen mutant F313C.	
XX			
KW	antibacterial; vaccine; protective antigen; PA; proteolytic degradation;		
KW	B.anthraxis toxin; B.anthraxis infection; passive immunisation;		
KW	inhalation anthrax; cutaneous anthrax; gastrointestinal anthrax; mutant;		
KW	mutin.		
OS	Bacillus anthracis.		
OS	Synthetic.		
XX			
XX	Key	location/Qualifiers	
FT	Misc-difference 313	/note= "wild type Phe substituted by Cys"	
FT			
FN	US2004171121-A1.		
XX			
PD	02-SEP-2004.		
XX			
XX	08-AUG-2003; 2003US-00638006.		
PF			
XX	09-AUG-2002; 2002US-0402285P.		
PR			
PA	(LEPP/) LEPPILA S H.		
PA	(ROSO/) ROSOVITZ M J.		
XX	(HSUS/) HSU S D.		
XX			
PI	Leppila SH, Rosovitz MJ, Hsu SD;		
DR	WPI; 2004-625107/60.		
XX			
PT	Novel Bacillus anthracis protective antigen having mutations conferring		
PT	enhanced resistance to proteolytic degradation compared to wild type		
PT	antigen, useful for inducing antibodies having neutralizing activity		
XX	anthrax toxin.		
XX			
PS	Claim 12; Page; 30pp; English.		
XX			
CC	The invention describes a recombinant Bacillus anthracis protective		

antigen (PA), modified to incorporate one or more mutations comprising an amino acid deletion or substitution in a flexible, exposed, or loop segment of the PA protein, where the one or more mutations confers enhanced resistance to proteolytic degradation compared to wild type PA. A pharmaceutical composition (I) comprising PA and physiologically acceptable carrier or a composition (II) comprising a synthetic construct encoding PA and a carrier is useful for inducing serum antibodies that have neutralising activity for a B.anthraxis toxin which involves administering (I) to a mammal (human), sufficient to elicit production of the antibodies. The antibodies protect the mammal against the infection. (I) is useful for vaccinating a human against B.anthraxis infection. An anti-PA-antibody containing composition is useful for passively immunising a mammal against the toxic effect of B.anthraxis. PA is useful as vaccines to induce serum antibodies which are useful to prevent, treat or reduced the severity of infections caused by B.anthraxis, such as inhalation anthrax, cutaneous anthrax and/or gastrointestinal anthrax. PA exhibits enhanced stability to proteolytic degradation that is increased by at least 25% compared to proteolytic stability of wild-type PA under comparable conditions. This is the amino acid sequence of protective antigen (PA) mutant F33C. Note: This sequence does not appear in the specification but has been created by the indexer using information given in the specification.

Query Match	96.4%	Score 3633	DB 8	Length 735
Best Local Similarity	97.0%	Pred. No. 5,4e-216		
Matches 713	Conservative 5	Matches 15	Indels 0	Gaps 0
QY	1	EVKQENRLNLSSESSSQGLGYYGFEDLNFQAPMVTSSSTTGGLSPSSSELENI	PSENOYF	60
DB	1	EVKQENRLNLSSESSSQGLGYYGFEDLNFQAPMVTSSSTTGGLSPSSSELENI	PSENOYF	60
QY	61	QSAIWSGFIKYKXSDERTFATSADNHTVMYDDQEVIMKASNSKIRLEKGLYQIKIYQ		120
DB	61	QSAIWSGFIKYKXSDERTFATSADNHTVMYDDQEVIMKASNSKIRLEKGLYQIKIYQ		120
QY	121	QRENPTEKGLPFKLYMTDSQNKKEVISSDNIQLPELKOKSSNSRKKRSTSAQPTVDRDN		180
DB	121	QRENPTEKGLPFKLYMTDSQNKKEVISSDNIQLPELKOKSSNSRKKRSTSAQPTVDRDN		180
QY	181	DGIDPSLEVEGYTDVKNKRTFLSPSWISNIHEKKGLTYKXSSPEKWSSTASDPYDPEKYT		240
DB	181	DGIDPSLEVEGYTDVKNKRTFLSPSWISNIHEKKGLTYKXSSPEKWSSTASDPYDPEKYT		240
QY	241	GRIDKNVSPEARHPVVAAPYPIVHDUMENIILSKNDSQNTQNDQSOTRTSKRTSRSDAN		300
DB	241	GRIDKNVSPEARHPVVAAPYPIVHDUMENIILSKNDSQNTQNDQSOTRTSKRTSRSDAN		300
QY	301	TVGVISISAGYQNGFTGNITTSAGFSNSNSTYALDHSLSLGERPMAETMGTLADTARL		360
DB	301	SEVHGNAVEHVASCFDIGGSVAGFSNSNSTYALDHSLSLGERPMAETMGTLADTARL		360
QY	361	NANIRYVNTGAPRIYNNULPTTSLVIGKQUTLATIAKENQOLSQIILAPNNYYSKQLAPIA		420
DB	361	NANIRYVNTGAPRIYNNULPTTSLVIGKQUTLATIAKENQOLSQIILAPNNYYSKQLAPIA		420
QY	421	LNADDDFSSTEITMNNYNOFLELEKTKQRLDQYGYAIATATNFENGRVRVDTGSNWSEV		480
DB	421	LNADDDFSSTEITMNNYNOFLELEKTKQRLDQYGYAIATATNFENGRVRVDTGSNWSEV		480
QY	481	LPQIOETTARILIFNGKDLNLVERRIIAVNPSPDELTTPYDMTLKEALKIAFGFNPNGUL		540
DB	481	LPQIOETTARILIFNGKDLNLVERRIIAVNPSPDELTTPYDMTLKEALKIAFGFNPNGUL		540
QY	541	QYGGDITEPDPENFPOQTSQNIKQOLAEIANTNTIYTVLADKIKLANXQNNILIDKKEFHYDR		600
DB	541	QYGGDITEPDPENFPOQTSQNIKQOLAEIANTNTIYTVLADKIKLANXQNNILIDKKEFHYDR		600
QY	601	NNIIVAGADESVYKKAHREVINSSTEGILLNLIKDKIRKLISGYAIEIDTEGKKEVINDRY		660
DB	601	NNIIVAGADESVYKKAHREVINSSTEGILLNLIKDKIRKLISGYAIEIDTEGKKEVINDRY		660

OY	661	DLNLSLRODGTPIIDFKXNDKLPYISNPNYKVNYAVTKENTIIINPSNGDSTNG	720
Db	661	DLNLSLRODGTPIIDFKXNDKLPYISNPNYKVNYAVTKENTIIINPSNGDSTNG	720
OY	721	IKKILIFSKGYEIG	735
Db	721	IKKILIFSKGYEIG	735

Search completed: August 11, 2006, 20:20:52
Job time : 212 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:17:36 ; Search time 307 Seconds
(without alignment)
2214.614 Million cell updates/sec

Title: US-10-780-250-1
Perfect score: 3770
Sequence: 1 EYKQENRLINESSESSQGL.....TSTNGIKKILIRSKKGYEIG 735

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2:*
1: uniprot_prot:*
2: uniprot_trembl:*

*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3634	96.4	736	068GS1_BACAN	068GS1 bacillus an
2	3634	96.4	764	1 PAG_BACAN	P13423 bacillus an
3	3634	96.4	764	052NR4_BACAN	052NR4 bacillus an
4	2744	72.8	561	042E94_BACAN	042E94 bacillus an
5	2140	56.8	760	04MW80_BACCE	04MW80 bacillus ce
6	984	26.1	875	046321_CLOPE	046321 clostridium
7	966.5	25.6	876	032739_CLODI	032739 clostridium
8	964.5	25.6	876	09KH41_CLODI	09KH41 clostridium
9	960.5	25.5	879	006498_9MOLU	006498 clostridium
10	829	22.0	721	086171_CLOBO	086171 clostridium
11	786	20.8	785	05JZY7_9BACL	05JZY7 brevibacill
12	776	20.6	871	05JZ26_9BACL	05JZ26 brevibacill
13	746	19.8	775	0844J8_BACTU	0844J8 bacillus th
14	296.5	7.9	225	1 Y6163_BACAN	P13422 bacillus an
15	232.5	6.2	1305	06FNZ8_CANGA	06FNZ8 candida gla
16	214	5.7	1723	07RQB6_PLAYO	07RQB6 plasmodium
17	213.5	5.7	1881	08RGK2_FUSNN	08RGK2 fusobacteri
18	211.5	5.6	1345	042IR6_PLABE	042IR6 plasmodium
19	209	5.5	4688	09P008_UREPA	09P008 ureplasma
20	204.5	5.4	2849	081HY4_PLAF7	081HY4 plasmodium
21	203	5.4	1227	097K41_CLOAB	097K41 clostridium
22	203	5.4	1965	02NFK4_9EURY	02NFK4 methanospa
23	202.5	5.4	1909	02NIC8_9EURY	02NIC8 methanospa
24	202.5	5.4	3759	02NRC4_PLAYO	02NRC4 plasmodium
25	201.5	5.3	2940	081RP9_PLAF7	081RP9 plasmodium
26	201.5	5.3	3119	07PES5_FUSNV	07PES5 fusobacteri
27	200.5	5.3	1904	081RS2_PLAF7	081RS2 plasmodium
28	200	5.3	920	07RLG3_PLAYO	07RLG3 plasmodium
29	199.5	5.3	2529	025579_HELPY	025579 heliobacte
30	199.5	5.3	2118	07RR57_PLAYO	07RR57 plasmodium
31	199.5	5.3	2331	068MS7_RICTY	068MS7 rickettsia

32	198.5	5.3	4095	2 Q7WZ13_HAESO	Q7WZ13 haemophilus
33	197.5	5.2	1461	2 Q7RAS6_PLAYO	Q7RAS6 plasmodium
34	197	5.2	1072	2 Q4Z640_PLABE	Q4Z640 plasmodium
35	197	5.2	3248	2 Q6LFP0_PLAF7	Q6LFP0 plasmodium
36	196	5.2	2169	2 Q7RHE7_PLAYO	Q7RHE7 plasmodium
37	196	5.2	2169	2 Q4ZHU0_STAHY	Q4ZHU0 staphylococ
38	196	5.2	10746	2 Q6GKX3_STMAR	Q6GKX3 staphylococ
39	195	5.2	2162	2 Q7RMF9_PLAYO	Q7RMF9 plasmodium
40	195	5.2	2719	2 Q7RPU0_PLAYO	Q7RPU0 plasmodium
41	194.5	5.2	1000	2 Q7RMA8_PLAYO	Q7RMA8 plasmodium
42	194.5	5.2	1873	2 Q6S003_DICDI	Q6S003 dicystocell
43	194	5.1	1444	2 Q7PDK0_PLAYO	Q7PDK0 plasmodium
44	194	5.1	1647	2 Q7RP46_PLAYO	Q7RP46 plasmodium
45	193.5	5.1	1231	2 Q7RT07_PLAYO	Q7RT07 plasmodium

ALIGNMENTS

RESULT 1
Q68GS1_BACAN PRELIMINARY, PRT; 736 AA.
ID Q68GS1;
AC Q68GS1;
DT 11-OCT-2004, integrated into UniprotKB/TREMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Protective antigen.
OS Bacillus anthracis.
OC Bacterioides, Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_Taxid=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Stemne;
RX PubMed=16030177;
RA Aziz M.A., Sikriwal D., Singh S., Jaryugla S., Kumar P.A.,
RA Bhattacharjee R.,
RT "Transformation of an edible crop with the paxa gene of Bacillus
RT anthracis".
RL FASEB J. 19:1501-1503 (2005).
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CC EMBL; AY700758; AAT98414.1; -; Genomic_DNA.
CC SMR; Q68GS1; 15-736.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR003896; Anthrax_toxinB.
DR InterPro; IPR011658; PA14.
DR InterPro; IPR013145; PA14_rel.
DR Pfam; PF03495; Binary_toxinB; 1.
DR Pfam; PF07691; PA14; 1.
DR PRINTS; PR01391; BINARYTOXINB.
KW plasmid.
SQ SEQUENCE 736 AA; 82805 MW; D2FF77A38AE372C CRC64;

Query Match 96.4%; Score 3634; DB 2; Length 736;
Best local similarity 97.2%; Pred. No. 1.9e-167;
Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

QY 1 EYKQENRLINESSESSQGLIGYFSDNLQAPMVVTSSTTGDLSTSSLENIIPSENQYF 60
DB 2 EYKQENRLINESSESSQGLIGYFSDNLQAPMVVTSSTTGDLSTSSLENIIPSENQYF 61
QY 61 QALNSGFLTKVKKSDYFATSDNHTVMVDDQEVYINKASNSNKRIRLTKGRLYQIKIQY 120
DB 62 QALNSGFLTKVKKSDYFATSDNHTVMVDDQEVYINKASNSNKRIRLTKGRLYQIKIQY 121
QY 121 QRENPEKGLDFKLWYVTSQNKKEVSISSDNLQPLBKQSSNSRKKRSTAGPTVDRDN 180
DB 122 QRENPEKGLDFKLWYVTSQNKKEVSISSDNLQPLBKQSSNSRKKRSTAGPTVDRDN 181

OY 181 DGIPDSLEVEGTTVDVKKRTFTLSPWISNIHEKGIITKYSPEKSTASDPYSPKXT 240
DB 182 DGIPDSLEVEGTTVDVKKRTFTLSPWISNIHEKGIITKYSPEKSTASDPYSPKXT 241
OY 241 GRIDGNVPEARHPVAAVPIYHVMMENIISKNEQSTONTDSQOTRTISKRTSQRDAN 300
DB 242 GRIDGNVPEARHPVAAVPIYHVMMENIISKNEQSTONTDSQOTRTISKRTSQRDAN 300
OY 301 TVGVSISAGYONGF--TGNITTSAGFSNSNSTVAIDHSLSLAGEKRTWAETMGLNTADT 357
DB 301 TSEVGNABVHASFIDIGSV--SAGFSNSNSTVAIDHSLSLAGEKRTWAETMGLNTADT 358
OY 358 ARLANINITYVTGTAPINVLPTTSLVIGKQTLATIRAKENQLSQIILAPNNYPSKXLA 417
DB 359 ARLANINITYVTGTAPINVLPTTSLVIGKQTLATIRAKENQLSQIILAPNNYPSKXLA 418
OY 418 PIALNAODFSSTPTTANNYNOFLAEKTKQALDPTDOYGNATATNFENGVRVDTGSNW 477
DB 419 PIALNAODFSSTPTTANNYNOFLAEKTKQALDPTDOYGNATATNFENGVRVDTGSNW 478
OY 478 SEVLFOIETTARIIENGKDLNVERRIAANVSPDLSTTKEDMTLKEALKIAGFNEPN 537
DB 479 SEVLFOIETTARIIENGKDLNVERRIAANVSPDLSTTKEDMTLKEALKIAGFNEPN 538
OY 538 GNLQYQGDITRPDPNPQOQSTONIKQALAEANATITVLDKILANAKMILLIDKRFH 597
DB 539 GNLQYQGDITRPDPNPQOQSTONIKQALAEANATITVLDKILANAKMILLIDKRFH 598
OY 598 YDRNNIANGADESVYKAEHREVINSTEGILNIDKIRKILSGYIVEIEDTEGKEYIN 657
DB 599 YDRNNIANGADESVYKAEHREVINSTEGILNIDKIRKILSGYIVEIEDTEGKEYIN 658
OY 658 DRYDMLNTSSLRQDGTFTIDFKKYNKCLPLYISNPNYKVVAVTKENTINSPENGDT 717
DB 659 DRYDMLNTSSLRQDGTFTIDFKKYNKCLPLYISNPNYKVVAVTKENTINSPENGDT 718
OY 718 TNGIRKILIFSKKGYEIG 735
DB 719 TNGIRKILIFSKKGYEIG 736

RESULT 2
PAGE_BACAN STANDARD, PRT: 764 AA.
AC P13423; Q937W2; Q9P5R7; Q9KH69; Q9R0U2;
DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
DT 18-OCT-2001, sequence version 2.
DT 07-MAR-2006, entry version 68.
DE Protective antigen precursor (PA) (PA-83) (PA83) (Anthrax toxin
translocating protein) [Contains: Protective antigen PA-20 (PA20);
Protective antigen PA-63 (PA63)].
GN Name=paga; Synonyms=pag;
Ordered locus names=pxo1-110, BXA0164, GBA0_pxo1_0164;
OS Bacillus anthracis.
OC Plasmid pxo1.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89172073; PubMed=3148491; DOI=10.1016/0378-1119(88)90439-8;
RA Welkos S.L., Lowe J.R., Eden-McCuchan F., Vodkin M., Leppla S.H.,
Schmidt J.J.;
RT "Sequence and analysis of the DNA encoding protective antigen of
Bacillus anthracis."
RL Gene 69:287-300(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX STRAIN=28, 33, BA1024, and BA1035;
MEDLINE=99214082; PubMed=10197966;
RA Price L.B., Hugh-Jones M., Jackson P.J., Keim P.;
RT "Genetic diversity in the protective antigen gene of Bacillus

RT anthracis.";
RL J. Bacteriol. 181:2358-2362(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX STRAIN=V770-NP1-R / ATCC 14185;
MEDLINE=20359347; PubMed=1089854;
DOI=10.1128/IAI.68.8.4549-4558.2000;
RA Cohen S., Mendelson I., Altboum Z., Kobiler D., Elhanany E., Bino T.,
Leitner M., Inbar I., Rosenberg H., Gozes Y., Bark R., Fisher M.,
Kotman C., Velan B., Shafrenman A.;
RT "Attenuated nontoxicogenic and nonencapsulated recombinant Bacillus
anthracis spore vaccines protect against anthrax."
RL Infect. Immun. 68:4549-4558(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Stemne;
RX MEDLINE=99445483; PubMed=10515943;
Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,
Martinez Y., Riche D., Svensson R., Jackson P.J.;
RT "Sequence and organization of pxo1, the large Bacillus anthracis
plasmid harboring the anthrax toxin genes."
RL J. Bacteriol. 181:6509-6515(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Ames / isolate Florida / A2012;
RX MEDLINE=22061436; PubMed=12004073; DOI=10.1126/science.1071837;
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Holtzapfel E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Frazer C.M.;
RT "Comparative genome sequencing for discovery of novel polymorphisms in
Bacillus anthracis."
RL Science 296:2028-2033(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames ancestor;
RA Rayel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Frazer C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 9-751.
RC STRAIN=Carbosap, and Ferrara;
RX MEDLINE=22063192; PubMed=12067380;
DOI=10.1046/j.1365-2672.2002.01660.x;
RA Adore R., Paeguali P., La Rosa G., Marinelli C., Muscillo M.,
Faenella A., Francia M., Ciuchini P.;
RT "Sequence analysis of the genes encoding for the major virulence
factors of Bacillus anthracis vaccine strain 'Carbosap'."
RL J. Appl. Microbiol. 93:117-121(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 195-434.
RC STRAIN=PA1;
RA Inoue S., Noguichi A., Tanabayashi K., Yamada A.;
RT "Preparation of a positive control DNA for molecular diagnosis of
Bacillus anthracis."
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [9]
RP DOMAINS.
RX MEDLINE=91332080; PubMed=1651334;
Singh Y., Klimpel K.R., Quinn C.P., Chaudhary V.K., Leppla S.H.;
RT "The carboxyl-terminal end of protective antigen is required for
receptor binding and anthrax toxin activity."
RL J. Biol. Chem. 266:15493-15497(1991).
RN [10]
RP CHARACTERIZATION.
RC STRAIN=Stemne;
RX MEDLINE=94327640; PubMed=8051159;
Milne J.C., Furlong D., Hanna P.C., Wall J.S., Collier R.J.;
RT "Anthrax protective antigen forms oligomers during intoxication of
mammalian cells."
RL J. Biol. Chem. 269:20607-20612(1994).

RP CHARACTERIZATION. Pubmed=11207581;
RX MEDLINE=21129592; Pubmed=11207581;
RX DOI=10.1046/j.1462-5822.2000.00052.x;
RA Beaugerard K.E., Collier R.J., Swanson J.A.;
RT "Proteolytic activation of receptor-bound anthrax protective antigen
RT on macrophages promotes its internalization.";
RL Cell. Microbiol. 2:251-258(2000).
RN (11)
RP TOXIN REGULATION.
RP STRAIN=Nebridge;
RX MEDLINE=94131936; Pubmed=8300513;
RA Koehler T.M., Dai Z., Kaufman-Varbray M.;
RT "Regulation of the Bacillus anthracis protective antigen gene: CO2 and
RT a trans-acting element activate transcription from one of two
RT promoters.";
RL J. Bacteriol. 176:586-595(1994).
RN (13)
RP FOLDING BY PSRA.
RX MEDLINE=22625622; Pubmed=12606539; DOI=10.1074/jbc.M301244200;
RX Williams R.C., Rees M.L., Jacobs M.F., Pragal Z., Thwaitte J.E.,
RA Baillie L.W., Emerson P.T., Harwood C.R.;
RT "Production of Bacillus anthracis protective antigen is dependent on
RT the extracellular chaperone, PrpA.";
RL J. Biol. Chem. 278:18056-18062(2003).
RN (14)
RP INTERACTION WITH THE ANTHRAX TOXIN RECEPTOR.
Pubmed=14507921; DOI=10.1074/jbc.M307900200;
RX Bradley K.A., Mogridge J., Jonah G., Rainey G.J.A., Batty S.,
RA Young J.A.T.;
RT "Binding of anthrax toxin to its receptor is similar to alpha
RT integrin-ligand interactions.";
RL J. Biol. Chem. 278:49342-49347(2003).
RN (15)
RP MUTAGENESIS OF PHE-342; PHE-343 AND ASP-344.
STRAIN=sterne;
RX MEDLINE=95050722; Pubmed=7961869; Shatma M., Leppia S.H.;
RA Singh Y., Klimpel K.R., Aroa N.;
RT "The chymotrypsin-sensitive site, PFD315, in anthrax toxin protective
RT antigen is required for translocation of lethal factor.";
RL J. Biol. Chem. 269:29039-29046(1994).
RN (16)
RP MUTAGENESIS OF DOMAINE 4 LOOPS.
STRAIN=sterne;
RX MEDLINE=99185012; Pubmed=10085028;
RA Varughese M., Teixeira A.V., Liu S., Leppia S.H.;
RT "Identification of a receptor-binding region within domain 4 of the
RT protective antigen component of anthrax toxin.";
RL Infect. Immun. 67:1860-1865(1999).
RN (17)
RP MUTAGENESIS OF TRP-375; MET-379 AND LEU-381.
STRAIN=sterne;
RX MEDLINE=21092804; Pubmed=11178978; DOI=10.1006/bbrc.2001.4320;
RA Batra S., Gupta P., Chaudhan V., Singh A., Bhatnagar R.;
RT "Trp 346 and Leu 352 residues in protective antigen are required for
RT the expression of anthrax lethal toxin activity.";
RL Biochem. Biophys. Res. Commun. 281:186-192(2001).
RN (18)
RP MUTAGENESIS OF PHE-581; PHE-583; ILE-591; LEU-595 AND ILE-603.
STRAIN=sterne;
RX MEDLINE=2138996; Pubmed=11554763; DOI=10.1006/bbrc.2001.5613;
RA Ahuja N., Kumar P., Bhatnagar R.;
RT "Hydrophobic residues Phe552, Phe554, Ile562, Leu566, and Ile574 are
RT required for oligomerization of anthrax protective antigen.";
RL Biochem. Biophys. Res. Commun. 287:542-549(2001).
RN (19)
RP MUTAGENESIS OF PRO-289.
STRAIN=sterne;
RX MEDLINE=21355689; Pubmed=11356563;
RA Khanna H., Chopra A.P., Aroa N., Chaudhry A., Singh Y.;
RT "Role of residues constituting the zbeta1 strand of domain II in the
RT biological activity of anthrax protective antigen.";
RL FEMS Microbiol. Lett. 199:27-31(2001).

RP (20)
RX MEDLINE=21125576; Pubmed=11222612;
RX DOI=10.1128/JB.183.6.2111-2116.2001;
RA Mogridge J., Mourez M., Collier R.J.;
RT "Involvement of domain 3 in oligomerization by the protective antigen
RT moiety of anthrax toxin.";
RL J. Bacteriol. 183:2111-2116(2001).
RN (21)
RP MUTAGENESIS OF LYS-426; ASP-454 AND PHE-456.
RX MEDLINE=21269403; Pubmed=11131126; DOI=10.1074/jbc.M008309200;
RA Sellman B.R., Nasai S., Collier R.J.;
RT "Point mutations in anthrax protective antigen that block
RT translocation.";
RL J. Biol. Chem. 276:8371-8376(2001).
RN (22)
RP MUTAGENESIS OF PRO-213; LEU-216; PHE-231; LEU-232; PRO-234; ILE-236;
RP ILE-239; TRP-255 AND PHE-265.
STRAIN=sterne;
RX MEDLINE=22112896; Pubmed=12117959;
RX DOI=10.1128/JAI.70.8.4477-4484.2002;
RA Chaudhan V., Bhatnagar R.;
RT "Identification of amino acid residues of anthrax protective antigen
RT involved in binding with lethal factor.";
RL Infect. Immun. 70:4477-4484(2002).
Query Match 96.4%; Score 3634; DB 1; Length 764;
Best Local Similarity 97.2%; Pred. No. 2e-167;
Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;
QY 1 EVKQENRLNSESSESSQGLGYFFSDNFOAPVWVTSSTTGDISSELENTPSSENOYF 60
DB 30 EVKQENRLNSESSESSQGLGYFFSDNFOAPVWVTSSTTGDISSELENTPSSENOYF 89
QY 61 QSAIWSGFIKVKKSDRYEATSDNHTVMWVDQEVINRASNKRLKRGRLYQIKIY 120
DB 90 QSAIWSGFIKVKKSDRYEATSDNHTVMWVDQEVINRASNKRLKRGRLYQIKIY 149
QY 121 QRENPFKGLDFKLYWTDSONKKEVTSNQLQPELKQKSSNRKRSISAGTVVDRDN 180
DB 150 QRENPFKGLDFKLYWTDSONKKEVTSNQLQPELKQKSSNRKRSISAGTVVDRDN 209
QY 181 DGIPOSLEVEGYTVQVKNKRTPLSPWISNIHEKGLTKKSSPEKSTSDPYSDPEKVT 240
DB 210 DGIPOSLEVEGYTVQVKNKRTPLSPWISNIHEKGLTKKSSPEKSTSDPYSDPEKVT 269
QY 241 GRIDKVSPEARHPPLVAAPYIVHVMENITLSKNEQSTQNTDSQRTTISKNTSRDAN 300
DB 270 GRIDKVSPEARHPPLVAAPYIVHVMENITLSKNEQSTQNTDSQRTTISKNTSR 328
QY 301 YGVGSISAGYQNGF--TGNITTSAGFSNNSSTVAIDHSLSLAGERTVAETWGLNTADT 357
DB 329 TSEVHGNALVHASFPDIGGSV--SAGFSNNSSTVAIDHSLSLAGERTVAETWGLNTADT 386
QY 358 ARLNANIRVYNGTAIYVVLPTSLVYGNKOTLAIKKNQSOILAPNNYPSKNLA 417
DB 387 ARLNANIRVYNGTAIYVVLPTSLVYGNKOTLAIKKNQSOILAPNNYPSKNLA 446
QY 418 PIALNAQDPSSPTITMANNOPLELEKTKQLRLDTPQVGNATYVFENGVRVVDGTSNW 477
DB 447 PIALNAQDPSSPTITMANNOPLELEKTKQLRLDTPQVGNATYVFENGVRVVDGTSNW 506
QY 478 SEVLPQIQETTAIIFNGKQNLVVERIAAVNPSDPLETTKPDMLKEALKIAFGNEEN 537
DB 507 SEVLPQIQETTAIIFNGKQNLVVERIAAVNPSDPLETTKPDMLKEALKIAFGNEEN 566
QY 538 GNLQYQGDITPDRFPDQTSQNTKNOCLAEINATYIVLTKIKANAMNIIIRKRF 597
DB 567 GNLQYQGDITPDRFPDQTSQNTKNOCLAEINATYIVLTKIKANAMNIIIRKRF 626
QY 598 YRRNNIAGVADSVVKEAREVINSSTEGILLINDKIRKILSGYIVLEDETEGLKEVIN 657
DB 627 YRRNNIAGVADSVVKEAREVINSSTEGILLINDKIRKILSGYIVLEDETEGLKEVIN 686


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QY 658 DRYMLNTSSLRQDKTPIIDPKKNDKLPYISNPNKYKNVYATKENTIIINPSENGDTS 717
DB 687 DRYMLNTSSLRQDKTPIIDPKKNDKLPYISNPNKYKNVYATKENTIIINPSENGDTS 746
QY 718 TNGIKKILIFSKKGYEIG 735
DB 747 TNGIKKILIFSKKGYEIG 764

RESULT 3
Q52NH4 BACAN PRELIMINARY; PRT; 764 AA.
ID Q52NH4 BACAN
AC Q52NH4
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Protective antigen.
GN Name: pag;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Al6R;
RA Xu J., Dong D., Chen W.;
RT "Protective antigen gene of Bacillus anthracis strain Al6R.";
RL Submitted (Apr-2005) to the EMBL/Genbank/DBJ databases.
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CC -----
EMBL: AY97299; AAY15236.1; -; Genomic_DNA.
SMR: Q52NH4; 43-764.
GO: GO:0005576; C:extracellular region; IEA.
GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR03896; Anthrax toxinB.
DR InterPro: IPR03145; PA14_toxI.
DR Pfam: PF03495; BimA14_toxI.
DR Pfam: PF07691; PA14_1.
DR PRINTS: PR01391; BINARYTOXINB.
SQ SEQUENCE 764 AA; 85811 MW; 3AB1BFBF48FAA03F CRC64;

Query Match 96.4%; Score 3634; DB 2; Length 764;
Beat Local Similarity 97.2%; Pred. No. 2e-167;
Matches 717; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

QY 1 EYKQENRLLNSESSESSOGLAGYFSDLNFOAPMVVTSSTTGDLSTPSELENIPEENQYF 60
DB 30 EYKQENRLLNSESSESSOGLAGYFSDLNFOAPMVVTSSTTGDLSTPSELENIPEENQYF 89
QY 61 QSAIWSGFIKVKXSDEYTFATSNADNHTVMVDDQEVINKANSNKIRLEKGLYQIKIY 120
DB 90 QSAIWSGFIKVKXSDEYTFATSNADNHTVMVDDQEVINKANSNKIRLEKGLYQIKIY 149
QY 121 QRENTTEKGLDKLYWTDSQNKKEVITSSNQLPELIKQSSNSRKKRSTASAPTPDDKN 180
DB 150 QRENTTEKGLDKLYWTDSQNKKEVITSSNQLPELIKQSSNSRKKRSTASAPTPDDKN 209
QY 181 DGIPSLSEVEGTYVVKKRTPLSPWISNIHEKGLTKYKSSPEKWSADSDYSPFEKYT 240
DB 210 DGIPSLSEVEGTYVVKKRTPLSPWISNIHEKGLTKYKSSPEKWSADSDYSPFEKYT 269
QY 241 GRIDKNSPEARHPVLAAYPIVHVDMENIIISKNDOSTONTDSQRTISKNTSTSRDAN 300
DB 270 GRIDKNSPEARHPVLAAYPIVHVDMENIIISKNDOSTONTDSQRTISKNTSTSR-TH 328
QY 301 TVGVYSISAGYQNGF--TGNITTSAGFSNSNSTYALIDHSLSLABERTVAELTGLTADT 357
DB 329 TSEVGNNAEVAHSPFDIGGSV--SAGFSNSNSTYALIDHSLSLABERTVAELTGLTADT 386
QY 358 ARLNANIRVNTGTAPIYVNVLPFTSLVLGKNGTQTLATIKAKENQGLQILAANNYPSKOLA 417
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DB 387 ARLNANIRVNTGTAPIYVNVLPFTSLVLGKNGTQTLATIKAKENQGLQILAANNYPSKOLA 446
QY 418 PIALNADDFSSPTITMNNYNOFLEKTKQRLDITDQYNGAIATYFENGVRVDYGSNW 477
DB 447 PIALNADDFSSPTITMNNYNOFLEKTKQRLDITDQYNGAIATYFENGVRVDYGSNW 506
QY 478 SEVLPOIOETIARILFNGKDLNVERRIAANPSDPLETTPEMDTLKALTIARGFNEPN 537
DB 507 SEVLPOIOETIARILFNGKDLNVERRIAANPSDPLETTPEMDTLKALTIARGFNEPN 566
QY 538 GNLQYQKDIPEFNPDOQTSQNIKNQALAEINATINYTVLDKIKLNAKQNIILRDKRFH 597
DB 567 GNLQYQKDIPEFNPDOQTSQNIKNQALAEINATINYTVLDKIKLNAKQNIILRDKRFH 626
QY 598 YDRNNIAVGADESYYKAEHREVINSSTEGLLNIDKDIRKILSGYIYEIEDTEGLKEVIN 657
DB 627 YDRNNIAVGADESYYKAEHREVINSSTEGLLNIDKDIRKILSGYIYEIEDTEGLKEVIN 686
QY 658 DRYMLNTSSLRQDKTPIIDPKKNDKLPYISNPNKYKNVYATKENTIIINPSENGDTS 717
DB 687 DRYMLNTSSLRQDKTPIIDPKKNDKLPYISNPNKYKNVYATKENTIIINPSENGDTS 746
QY 718 TNGIKKILIFSKKGYEIG 735
DB 747 TNGIKKILIFSKKGYEIG 764

RESULT 4
Q4ZE94 BACAN PRELIMINARY; PRT; 561 AA.
ID Q4ZE94 BACAN
AC Q4ZE94
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Protective antigen (Fragment).
GN Name: pa;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=34F2;
RA Vahedi F., Moazeni Julia G., Mahmoudi M.;
RT "Humoral immunity in mice induced by vaccination with a plasmid
RT encoding anthrax protective antigen.";
RL Submitted (Feb-2005) to the EMBL/Genbank/DBJ databases.
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EMBL: AY921578; AAX84029.1; -; Genomic_DNA.
SMR: Q4ZE94; 1-561.
GO: GO:0005576; C:extracellular region; IEA.
GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR03896; Anthrax toxinB.
DR Pfam: PF03495; BimA14_toxI.
DR PRINTS: PR01391; BINARYTOXINB.
KW Plasmid.
KW NON TER.
SQ SEQUENCE 561 AA; 62846 MW; 88D32AACDF5955FA CRC64;

Query Match 72.8%; Score 2744; DB 2; Length 561;
Beat Local Similarity 96.3%; Pred. No. 1.4e-124;
Matches 543; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

QY 175 VPDNDNGIIPSLSEVEGTYVVKKRTPLSPWISNIHEKGLTKYKSSPEKWSADSDYS 234
DB 1 VPDNDNGIIPSLSEVEGTYVVKKRTPLSPWISNIHEKGLTKYKSSPEKWSADSDYS 60
QY 235 DPEKVTGRIDKNSPEARHPVLAAYPIVHVDMENIIISKNDOSTONTDSQRTISKNTS 294
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DB 61 DEKVTGRIDKNVSPARHPVLAAPVIVHDMENILLSKNEOSTQNTISQRTIKKNS 120
QY 295 TSDANTVGVSIAGYQNF---TGNITTSAGFSNNSSTVAIDHSISLAGEWTAEWG 351
DB 121 TTR-THTSEVHGNAAVHAFPDIGSV--SAGFSNNSSTVAIDHSISLAGEWTAEWG 177
QY 352 LMTADTARLANINIRYNTGTAPRYNVLPTTSLVIGKQOTLATIKAKENQISQILAPNNTY 411
DB 178 LMTADTARLANINIRYNTGTAPRYNVLPTTSLVIGKQOTLATIKAKENQISQILAPNNTY 237
QY 412 PSKNLAPILANQDDSSPTITNNVNOFLEKTKQLRLDTPQVGNIAVTYENGRVAV 471
DB 238 PSKNLAPILANQDDSSPTITNNVNOFLEKTKQLRLDTPQVGNIAVTYENGRVAV 297
QY 472 DTGSNNSEVLPOIQTETARIIFNGKDLNVERRIAANPSDPLETTKPDMLTKALKIAP 531
DB 298 DTGSNNSEVLPOIQTETARIIFNGKDLNVERRIAANPSDPLETTKPDMLTKALKIAP 357
QY 532 GENEPMNGNTQYQKDIITEFDNFDOQTSQNIKNQALAEIANTYIVLDKIKLAKANNILI 591
DB 358 GENEPMNGNTQYQKDIITEFDNFDOQTSQNIKNQALAEIANTYIVLDKIKLAKANNILI 417
QY 592 RKRRTFYDNNNTAVGADSEVYKAEHREVINSSTEGILLNIDKDIRKILSGYVEIEDTG 651
DB 418 RKRRTFYDNNNTAVGADSEVYKAEHREVINSSTEGILLNIDKDIRKILSGYVEIEDTG 477
QY 652 LKEVINDRYDMLNISLRQDKTFIDFKKYNDCLPLYISNPNKYVAVYATKENTIIINS 711
DB 478 LKEVINDRYDMLNISLRQDKTFIDFKKYNDCLPLYISNPNKYVAVYATKENTIIINS 537
QY 712 ENGDTSTNGIKKILIFSKKGYEIG 735
DB 538 ENGDTSTNGIKKILIFSKKGYEIG 561

RESULT 5
Q46221_BACCE PRELIMINARY; PRT; 760 AA.
ID Q46221_BACCE PRELIMINARY; PRT; 760 AA.
AC Q46221_BACCE PRELIMINARY; PRT; 760 AA.
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Protective antigen.
ORFNames=BCE G9241_PBC218_0026;
OS Bacillus cereus G9241.
OC plasmid pBC218
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
NCBI_TaxID=269801;
[1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RC PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Maieron C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Rilestone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.,
RT Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax."
RT Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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EMBL: AABK0100004; EAL15944.1; -; Genomic DNA.
DR GO: GO:000576; C:extracellular region; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR003896; Anthrax_toxinB.

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DR InterPro: IPR033145; PA14_rel.
DR Pfam: PF03495; Binary_toxinB.
DR Pfam: PF07691; PA14_1.
DR PRINTS: PR01391; BINARYTOXINB.
DR plasmid.
SQ SEQUENCE 760 AA; 85765 MW; 7488F5E5B5F1F054 CRC64;

Query Match 56.8%; Score 2140; DB 2; Length 760;
Best Local Similarity 58.3%; Pred. No. 3.4e-95;
Matches 427; Conservative 118; Mismatches 177; Indels 10; Gaps 7;

QY 4 QENRLNESESSQGLGYFSDINLQAPMVVTSSTTGLSIPSSLEN-IPSENOYFOS 62
DB 33 QEDSLIQGKETSQGLGYFSDINLQAPMVVTSSTTGLSIPSSLEN-IPSENOYFOS 92
QY 63 AIMSFGIKYKKSDEYTFATSDNNHVTMVDQEVINKASNSKIRLEKRLQIKIYQYR 122
DB 93 AIMSFGIKYKKSDEYTFATSDNNHVTMVDQEVINKASNSKIRLEKRLQIKIYQYR 152
QY 123 ENPTEKGLDPKLYWDSQKKEVYSSDNIQLPELKQKSSNSRKRSTAGPTVPKRDNDG 182
DB 153 ESPSEKGIQFOLYWTTPDWTTEITPKSKLLPLPKAKSSKSTERSANNRREIVSDNDG 212
QY 183 IPDSLEVEGYVDVKNKRTFELSPWISNIEKKGLATYKSSPEKMSYASDPYDFEKYVGR 242
DB 213 IPDSLEVEGYVDVKNKRTFELSPWISNIEKKGLATYKSSPEKMSYASDPYDFEKYVGR 272
QY 243 IDKNVSPARHPVLAAPVIVHDMENILLSKNEOSTQNTISQRTIKKNSRSD--A 299
DB 273 IDKNVSPARHPVLAAPVIVHDMENILLSKNEOSTQNTISQRTIKKNSRSD--A 332
QY 300 NTYGVSIAGYQNFNGNTTSAGFSNNSSTVAIDHSISLAGEWTAEWGTLADTAR 359
DB 333 NTYGVSIAGYQNFNGNTTSAGFSNNSSTVAIDHSISLAGEWTAEWGTLADTAR 389
QY 360 LMANIRYNTGTAPRYNVLPTTSLVIGKQOTLATIKAKENQISQILAPNNTY 419
DB 390 LMANIRYNTGTAPRYNVLPTTSLVIGKQOTLATIKAKENQISQILAPNNTY 449
QY 420 ALNAQDDFSTPTITNNVNOFLEKTKQLRLDTPQVGNIAVTYENGRVAVDTGSNNSE 479
DB 450 ALNAQDDFSTPTITNNVNOFLEKTKQLRLDTPQVGNIAVTYENGRVAVDTGSNNSE 509
QY 480 VLPQIQTETARIIFNGKDLNVERRIAANPSDPLETTKPDMLTKALKIAPFPNPNXN 539
DB 510 VLPQIQTETARIIFNGKDLNVERRIAANPSDPLETTKPDMLTKALKIAPFPNPNXN 569
QY 540 LQYQKDIITEFDNFDOQTSQNIKNQALAEIANTYIVLDKIKLAKANNILI 599
DB 570 LQYQKDIITEFDNFDOQTSQNIKNQALAEIANTYIVLDKIKLAKANNILI 628
QY 600 RNNIAGADESVYKAEHREVINSSTEGILLNIDKDIRKILSGYVEIEDTGKEVINDR 659
DB 629 RNNIAGADESVYKAEHREVINSSTEGILLNIDKDIRKILSGYVEIEDTGKEVINDR 688
QY 660 YDMLANISSLRQDKTFIDFKKYNDCLPLYISNPNKYVAVYATKENTIIINSNGTSTN 719
DB 689 YDMLANISSLRQDKTFIDFKKYNDCLPLYISNPNKYVAVYATKENTIIINSNGTSTN 747
QY 720 GIKK-ILIFSK 730
DB 748 DSEKGLVLSLK 759

RESULT 6
Q46221_CLOPE PRELIMINARY; PRT; 875 AA.
ID Q46221_CLOPE PRELIMINARY; PRT; 875 AA.
AC Q46221_CLOPE PRELIMINARY; PRT; 875 AA.
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Toxin component of Bacillus anthracis spore.
OS Clostridium perfringens.

```

[illegible]

D6		: : : : : : :	478	ETTOSAGNYGTRK-SQGOI-ITTEGNSMNTISQSDVSASIIID-TSGQTERRVAAKEO	534
OY		511 SDPLETTKPDWTLKEALKAIEFNEPENGNIQY-OQKDITE--FDNFPOQSONIKNOLA	567		
D6		535 GNPDCKT-PEITIGEAIKKAPSATK-NGEILLYFNGIPIDESCVELIFDDNTESEIIKEQLK	592		
OY		568 ELANNTIYTULDKTKLNAKNMILLRDKRF-HYDR-INNIANGADESVVKEHREVINST	624		
D6		593 YLDPRKIYNV---KLBRGNMILLKVPSYFTNFDEYNFP--AASWSNIDTYKNODLOSAVA	646		
OY		625 EGL-----LINIPDKDIRKILSGY-----IVBIEDEGLEKVINDEYDMINI	665		
D6		647 NKLSGETKIITPMKLAPEYKYRYVSSGSKDPSTNSITVNKSQEOKTDYLVPBKDYTKF	706		
OY		666 S-----SLRODGKTFFIDPKXYND-KLPYLIASNPNKYX-----N	697		
D6		707 SYEFETTGKDSIDIBILTSTSGVAFLDNLSTEINSPFEILKEBEIKVPDQEIILDANH	766		
OY		698 VYAVTKENTTIINPSENGDTSTNGI	721		
D6		767 YYADIKLDT-----NTGNTYIDGI	785		
 RESULT 7 032739_CLODI ID 032739_CLODI PRELIMINARY; PRT; 876 AA. AC 032739; DT 01-JAN-1998, integrated into UniProtKB/TrEMBL. DT 01-JAN-1998, sequence version 1. DT 07-FEB-2006, entry version 22. DE ADP-ribosyltransferase. GN Name=cdtbg; OS Clostridium difficile. OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; CC Clostridium. CX NCBI_TaxID=1496; RN [1] RP NOCLBOTIDE SEQUENCE. RC STRAIN=CDI196; RX MEDLINE=97230316; PubMed=9119480; RA Perelle S., Gilbert M., Bourloux P., Corthier G., Popoff M.R.; RT "Production of a complete binary toxin (actin-specific ADP- riboyltransferase) by Clostridium difficile CD196."; RL Infect. Immun. 65:1402-1407(1997). CC CC CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms CC Distributed under the Creative Commons Attribution-NoDerivs license ----- CC EMBL; L76081; AAB67305.1; -; Genomic DNA. DR HSBP; P13423; IACC. DR GO; GO:0005576; C:extracellular region; IEA. DR GO; GO:0016740; F:transferase activity; IEA. DR GO; GO:0009405; P:pathogenesis; IEA. DR InterPro; IPRO03896; Anthrax_toxinB. DR InterPro; IPRO11658; PA14. DR InterPro; IPRO13145; PA14_rel. DR Pfam; PF03495; Binary_toxB; 1. DR Pfam; PF07691; PA14; 1. DR PRINTS; PR01391; BINARXTOXINB. KW Transferase. SQ SEQUENCE 876 AA; 98797 MW; 25E06E2D45CE2B3B CRC64; Query Match 25.6%; Score 966.5; DB 2; Length 876; Best Local Similarity 33.8%; Pred. No. 2,3e-38; Matches 266; Conservative 137; Mismatches 274; Indels 111; Gaps 31.					
OY		4 QENRLINESSSQGELGYFSDFNPQAPMVVTSTTGDISIPSELEN-IPSENQYROS	62		
D6		40 KKKELVIEDLLPNNGKMGVYFSDHPFKDLKLMADIKOENLKFEERKVDKLDKDKSDVKS	99		
OY		63 ALMSGFIKVKSDSYTPATSADNVHTVVVDQEVINTASNSNKIRLEGRGLYQIKIQYOR	122		

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Db 100 IRWTGRIIPSKOGEYTLSTDRD-VLMQVNTBSTI---SNTLKVNNKKGKRYRIELOD 155
Qy 123 EN--PTEKGLDFLYTDSQNKKEVISDNLOPELKQKSSNRKRKSTAGTVP---- 176
Db 156 KNLGSIIDNLSPPLYM-ELDGKKKIIPENLFLRDY----SNIEKD-----DPIFIPNNF 205
Qy 177 -----DDNDGIPDLSLEVEGYTVVKNKRTFLSMISNHEKKGLTYKXS 222
Db 206 FDPKMSDWEDEDLTDNDNIPDSYERNGTI---KDLIAVMEDESPAE-QGYKXYVSN 260
Qy 223 PEKMTASDPYSPDEFKVTGRIDKNVSEAPRPLVAAYPIVHVDMENIISKNDOSTONT 282
Db 261 YLESNTAGDPDYTYEKASGSFDFKAITKEARDPLVAAPIVGVMEKLIISTNHAST--- 317
Qy 283 DSQRTISKNSTSR--DANTVGVISAGYONGFTGNITTSAGSNNSTVAIDHSLSLA 341
Db 318 -DQKTVSBAITNSKTESNTAGVSVMVYONGFTAVNTVYSHTTDNSTAVQDSN----- 371
Qy 342 GERTMAETGLTADTARLANANIRYNTGTAPLYNVLPTTSVLGKNGTLATIKAKENOL 401
Db 372 GE-SMWTGLSINGESAYINANRYNTGTAPMYKVTPTNLVL-DGDTLSTIKAOENOT 429
Qy 402 SQTLLANNYPSKQLAPIALNAODDFSTPTTNVNOFLEKTKQLRLDPTDQVYGNIAI 461
Db 430 GNNLSFGDYTPKKGLSPLALNTMDQSSRLIPINYOQLKLDGKQIKLETTOVSGNFGT 489
Qy 462 YNEENGRVAVDTGSNNSEVLPOIQTETARIIFNGKDLNVERRIAANVPSDPLETTKPM 521
Db 490 KN-SSGQI-VTEGNSMDVYISQIDSISASIIIDTEN-BSEYRVTAKNLODPEDKT-PEL 545
Qy 522 TLKALKIAFGNEPENGLOYGKDIITE--FDNFPQOQTSQNIKNQLABLANATNIYTVLD 579
Db 546 TIGEAIEKAFATKQGLLYFNDDIPIDESCVLELIPDNTANKIKDSLKTLSDKKIYV-- 603
Qy 580 KIKLANKNLILDRKRFHY---DRNNIAGADESVYKHAHRYVNSTEGL----- 627
Db 604 --KLERGMNLIKTPYFTNPDYNNYP--STWSNVNTTNQDGLQSSANKLNETKIKIP 659
Qy 628 LNLNDKDIRKILSGY-----IVEI-----EDTEGL-----KEVINDRYDML 663
Db 660 MSBLKPKRYKRVFSGYSKDPJLTSNSIIYKIKAKEBKTDYLVPEQGYTKFSYEPETEKDS 719
Qy 664 NIS-SLRQDKTIFDEKTYND--KLPLYISNPNYK-----VNTVAVTKENTINPSEN 713
Db 720 NIEITLIGSGTYLDMLSITELNSTPEILDEBEVKIPTDQEIINDAHKIYPADLNFPNS-T 778
Qy 714 GDTSTNGI 721
Db 779 GNTYINGM 786

RESULT 8
09KH41_CLODI PRELIMINARY; PRT; 876 AA.
AC 09KH41;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Cdb.
GN Name=cdb;
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_Taxid=1496;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CCUG 20309;
RA MEDLINE=21604263; PubMed=11761709;
RX Chang S.Y., Song K.P.;
RT "ADP-ribosylating binary toxin genes of Clostridium difficile strain
CCUG 20309."
RL DNA Seq. 12:115-120(2001).
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CC -----
CC EMBL; AF271719; AAF81761.1; -, Genomic_DNA.
CC HSSP; P13423; IACC.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR003896; Anthrax_toxinB.
DR InterPro; IPR011658; PA14.
DR InterPro; IPR013145; PA14_rel.
DR Pfam; PF03495; Binary_toxib.
DR Pfam; PF07691; PA14_1.
DR PRINTS; PR01391; BINARYTOXINB.
SQ SEQUENCE 876 AA; 98793 MW; 366D62F352B745A5 CRC64;

Query Match 25.6%; Score 964.5; DB 2; Length 876;
Best Local Similarity 33.6%; Pred. No. 2,9e-38;
Matches 265; Conservative 138; Mismatches 274; Indels 111; Gaps 31;

Qy 4 QENRLANSESSSQGLGYTFPSDLPQAPVWYTSSTGDLSPSSLEN-IPENGYFQS 62
Db 40 KKKEIVNEDILPNNGLMGYTFDEHPKDLKMAPIKGNLKREKKVDKLDKQSDVKS 99
Qy 63 AMSGFIKVKKSDYETPATSADNHYTMVYDDQEVINKASNKRIRLEKGLYOIKIYOQR 122
Db 100 IRWTGRIIPSKOGEYTLSTDRD-VLMQVNTBSTI---SNTLKVNNKKGKRYRIELOD 155
Qy 123 EN--PTEKGLDFLYTDSQNKKEVISDNLOPELKQKSSNRKRKSTAGTVP---- 176
Db 156 KNLGSIIDNLSPPLYM-ELDGKKKIIPENLFLRDY----SNIEKD-----DPIFIPNNF 205
Qy 177 -----DDNDGIPDLSLEVEGYTVVKNKRTFLSMISNHEKKGLTYKXS 222
Db 206 FDPKMSDWEDEDLTDNDNIPDSYERNGTI---KDLIAVMEDESPAE-QGYKXYVSN 260
Qy 223 PEKMTASDPYSPDEFKVTGRIDKNVSEAPRPLVAAYPIVHVDMENIISKNDOSTONT 282
Db 261 YLESNTAGDPDYTYEKASGSFDFKAITKEARDPLVAAPIVGVMEKLIISTNHAST--- 317
Qy 283 DSQRTISKNSTSR--DANTVGVISAGYONGFTGNITTSAGSNNSTVAIDHSLSLA 341
Db 318 -DQKTVSBAITNSKTESNTAGVSVMVYONGFTAVNTVYSHTTDNSTAVQDSN----- 371
Qy 342 GERTMAETGLTADTARLANANIRYNTGTAPLYNVLPTTSVLGKNGTLATIKAKENOL 401
Db 372 GE-SMWTGLSINGESAYINANRYNTGTAPMYKVTPTNLVL-DGDTLSTIKAOENOT 429
Qy 402 SQTLLANNYPSKQLAPIALNAODDFSTPTTNVNOFLEKTKQLRLDPTDQVYGNIAI 461
Db 430 GNNLSFGDYTPKKGLSPLALNTMDQSSRLIPINYOQLKLDGKQIKLETTOVSGNFGT 489
Qy 462 YNEENGRVAVDTGSNNSEVLPOIQTETARIIFNGKDLNVERRIAANVPSDPLETTKPM 521
Db 490 KN-SSGQI-VTEGNSMDVYISQIDSISASIIIDTEN-BSEYRVTAKNLODPEDKT-PEL 545
Qy 522 TLKALKIAFGNEPENGLOYGKDIITE--FDNFPQOQTSQNIKNQLABLANATNIYTVLD 579
Db 546 TIGEAIEKAFATKQGLLYFNDDIPIDESCVLELIPDNTANKIKDSLKTLSDKKIYV-- 603
Qy 580 KIKLANKNLILDRKRFHY---DRNNIAGADESVYKHAHRYVNSTEGL----- 627
Db 604 --KLERGMNLIKTPYFTNPDYNNYP--STWSNVNTTNQDGLQSSANKLNETKIKIP 659
Qy 628 LNLNDKDIRKILSGY-----IVEI-----EDTEGL-----KEVINDRYDML 663
Db 660 MSBLKPKRYKRVFSGYSKDPJLTSNSIIYKIKAKEBKTDYLVPEQGYTKFSYEPETEKDS 719
Qy 664 NIS-SLRQDKTIFDEKTYND--KLPLYISNPNYK-----VNTVAVTKENTINPSEN 713
Db 720 NIEITLIGSGTYLDMLSITELNSTPEILDEBEVKIPTDQEIINDAHKIYPADLNFPNS-T 778
Qy 714 GDTSTNGI 721
Db 714 GDTSTNGI 721
| | | |
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Db 779 GNTYINGM 786

RESULT 9

ID 006498_9MOLU PRELIMINARY; PRT; 879 AA.

AC 006498;

DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.

DT 01-JUL-1997, sequence version 1.

DT 07-FEB-2006, entry version 23.

DE Sb component.

DE Name=Sbs;

OS Clostridium spiroforme.

OC Bacteria; Firmicutes; Mollicutes.

OX NCBI_TaxID=29348;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CS246;

RA Gilbert M., Perelle S., Daube G., Popoff M.R.;

RT "Clostridium spiroforme toxin genes are related to C. perfringens iota toxin genes but have a different genomic localization.";

RT Syst. Appl. Microbiol. 20:337-347(1997).

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CC -----

EMBL: X97969; CA66612.1; -; Genomic_DNA.

DR HSP; P13423; IACC.

DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR003896; Anthrax_toxinB.

DR InterPro; IPR013145; PA14.

DR InterPro; IPR013145; PA14_rel.

DR Pfam; PF03495; Binary_toxB; 1.

DR Pfam; PF07691; PA14; 1.

DR PRINTS; PR01391; BINARYTOXINB.

DR SEQUENCE 879 AA; 98739 MW; 4065ACB8E05BA01 CRC64;

Query Match 25.5%; Score 960.5; DB 2; Length 879;

Best Local Similarity 30.2%; Pred. No. 4,5e-38;

Matches 272; Conservative 146; Mismatches 248; Indels 235; Gaps 34;

QY 4 QENRLNSESSESGILGYFSDLNFOAMVVTSTTGDLSPSELENIPENQ-YFQS 62

DB 36 QEVETNTEKTVSSNGMGTTFADHFKEIEMAPYKNGELKPKKVEKLTTEKTNKS 95

QY 63 AIWSGFIKVKSDSEYFATSDNHYTMWVDQEVINKASNKIRLEKRLYQIKIYOR 122

DB 96 IRMTGRILIPSKQGEYTLSTDKN-VLMQINAE--GEIANTLKVMIKQGEYSIRIEQ- 150

QY 123 ENPTREKGLDF-----KLYWTDSONKKEVISDNILQPELKQKSN----- 162

DB 151 ---PKDIGYVDLSPPKLYW-ELMGDKTLIPKMKLFADYSKIDENPPIPKDNFFDLK 205

QY 153 --SRKKRSTSA-GPYVPDRDNDGIPDSLEVEGYTVDKNKRFFLSPWISNHEKKGLTKY 219

DB 206 LKSRARLARGWDEBDDLTDDNNIPAYEKNGTIT--KDSIAYKW-EDSPAQGYKKY 260

QY 220 KSSPEKWSIADSPYSDPEFYKTRIDKNVSPKARHPLVLAAYPIVHYDMENIILSKNEDST 279

DB 261 LSSYLESNATGAPPYDYQKASGSPKAIQAEARDPLVAAYPVGVGMKELIISTHEHAST 320

QY 280 QNTDSQRTTISKNTSTR-DANTGVGVSISAGYQNGFTGNTTSAGFSNSNSTVAIDHSL 338

DB 321 ---DQKTVSHATTNKTSDANTAGVAINIAYQNGFTGSIITN--YSHTEENSTAVQNS- 373

QY 339 SIAGRTAETMGTLADTARLANRNVNRTGAPTYANVLPTTSIVLGNQGLATIKAKE 398

DB 374 --NGR-SMWTSLINKEGSAVINANRNYNTGAPRYKATPTTNLVL-DGDTLVTTIKAD 429

QY 399 NQLSQILAPNNYPSKNTLAPIALNADDDPSSTPTTWYNTQPLEKTKQLRLDTPQVYGN 458

DB 430 NQIGNNLSNENYPPKGLSPALNMTDQSSRLIPINTYQLKKLDAGKQIKLETTQVSN 489

QY 459 IATYFENGVRVDT-GSMGEVLPOIQTETARITFN-GKDLNVERRIAAVNSDPLET 516

DB 490 ---YGIKNSQGIITTEGNSWSDYISQIDSLASIIIDQSD--VFERVATKSDSNPBDK 544

QY 517 TKPDMTLKEALKIAFGFNEPNGNIQYQCKDYTE--FDENPDQOSTONIKQDLAEINATNI 574

DB 545 T-PVLTIGEALEKAFGATKNGEILYFNQMPIDESCVELIPGNTANLIKERLINALNDKKI 603

QY 575 YTVLDKTLGNKNNILIRD----- 593

DB 604 YNV-----QIERGMKILIXTSTYFNNPDGYNPPSSWSNVDSNODGLQNAANKLSGETYI 659

QY 594 -----KRFHY----- 598

DB 660 VIPMSKLNPRYRYPSSGLKNSSTSNPTTNVIAKAEQKTYNLVSENDYKKTSTYERITGR 719

QY 599 DRNN-----IAGDAESVYKAREV-----IN 621

DB 720 DASNIETLTSSGTLFLDNLSTELNSTPEILKEPDIKVPDQELI-DAHKKYADLSFN 778

QY 622 STTEGLIN-----IDKIRKILSGIYEIE-DTBGLKEVINDRIDMANTISLRQDG 672

DB 779 QSTANYVLDGLYFEPYQTNKEVLDYIQKYKVEATLEYSGFQDGTGKKELENNYGDSONQ 838

QY 673 KT-FIDFKYNDKLPLYISNPNY---KVNYYAVTKENTINPSENGDPTNGIKILIF 727

DB 839 KINYVNFSTY-----FTSGENWMPYKGRITYALTPEH-----KELLVL 876

QY 728 S 728

DB 877 S 877

RESULT 10

ID 086171_CLOBO PRELIMINARY; PRT; 721 AA.

AC 086171-

DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.

DT 01-NOV-1998, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE C2 toxin (Component-II).

OS Clostridium botulinum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

OX NCBI_TaxID=1491;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN-type C;

RX MEDLINE=96184657; PubMed=8645309; DOI=10.1006/bbrc.1996.0409;

RA Fujii N., Kubota T., Shirakawa S., Kimura K., Ohishi I., Morishishi K., Isogai E., Isogai H.;

RT "Characterization of component-I gene of botulinum C2 toxin and PCR detection of its gene in clostridial species.";

RT Biochem. Biophys. Res. Commun. 220:353-359(1996).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN-type C;

RX MEDLINE=96323874; PubMed=9659689; DOI=10.1016/S0378-1135(98)00195-3;

RA Kimura K., Kubota T., Ohishi I., Isogai H., Isogai E., Fujii N.;

RT "The gene for component-II of botulinum C2 toxin.";

RT Vet. Microbiol. 62:27-34(1998).

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CC -----

EMBL: D88982; BAA32537.1; -; Genomic_DNA.

DR HSP; P13423; IACC.

DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR003896; Anthrax_toxinB.

DR InterPro; IPR013145; PA14.

DR InterPro; IPR013145; PA14_rel.

DR Pfam: PR03495; Binary toxB; 1.
DR Pfam: PR07691; PA14; 1.
DR PRINTS; PR01391; BINARYTOXB.
SQ SEQUENCE 721 AA; 80516 MW; 44C8153AC7A9D5F2 CRC64;
Query Match 22.0%; Score 829; DB 2; Length 721;
Best local Similarity 35.4%; Pred. No. 8e-32;
Matches 224; Conservative 120; Mismatches 224; Indels 64; Gaps 26;
QY 3 KOENRLNSES--SSQGLIGYFSDLNFAQPMVYTSSTTGDLSIPSSLENIIPSENGYF 60
DB 5 KENSIVSNKNKYFTINGLMGYFEN--DFENIIISPTLDGNLTFSEKDINSILG--NKII 62
QY 61 QSAINGCFIKYKSDYTPATSDN--HYTMVDQVINKAS--SKIKLEKRLVQIKI 118
DB 63 KSARMIGLIPSTIGYIISTSSPNCRVEL--NGEIFNLISLTSNTVNLIQSNVYDI 119
QY 119 -QYORENPTKGLD--FKLYWTDSONKKEVISDNLOPELKOKSNSRKRKSTASAPY- 175
DB 120 EQLMSNQLLKRYEGIKLYWETSIDIKEIIPSEVL--LKPYVSTNTEKSKRTIPNITLF 175
QY 176 -----PRNDNGIPDSLEVEGYTDVKNKRTFLSPWISNIHEKKGLTRYKSPK 225
DB 176 SNAKLANANRDTDRDGIPEWEINGYTMNQKAVAMDKFAAN-----GYKKYVSNPK 230
QY 226 WSTASDPYDFEKTGRIDKNVSPKARHPLVAAPYIVHYDMENIISKNEDOSNTDQ 285
DB 231 PCTANDPYDFEKTGRIDKNVSPKARHPLVAAPYIVHYDMENIISKNEDOSNTDQ 286
QY 286 TTTISKNTS--TSRDATVGVISAGVNGPTGNI-----TTSAGFSNSSTVAIDHSI 338
DB 287 TTSMSSTHSSTHSNITVGAESVSLD--LAGGIPIVPSKMSASANTSHWTONTSTYDDT- 343
QY 339 SLAGEETMAETMGLNADTARLANIRYVNTGTAPYVNLPTTSLVIGKNOGLATTIKAK 398
DB 344 --TGE--SFQSGISINTGESAYINPIRYVNTGTAPYVNLPTTITVIDK--QSAVATIKGE 399
QY 399 NQLSQTLPANNYPKSNLAPIALNADDFSTPTMTNNOFLEKTKQLRLDTPQYGN 458
DB 400 SLIGDIANFGGYPIIGEPFPMALNTMDQFSRLPIPNYNOLKSIDGQYTMSTSQFTGN 459
QY 459 IATYVNEGRVAVDNGSNSEVLPOIQTARTI--FNGKDLNVERRIAANVPSDPLET 516
DB 460 FAKTN--SNANLVTD--GNMNGPYITIKSTTASLTLSFSQGTQVA--VVAEPSPDEK 514
QY 517 TTPDMTLKALKIAFGNEPNGNLQYQKQDIT--EFDNFQDOTSQNIKNOLELNATN 573
DB 515 T-PKLTLEQALVKAFLBKNGKGFYHGLEISKNEKIQVFLDSNTNNDPENQKXNTADQ 573
QY 574 IYTVLDKIKLANAKNILLRDKRFHYDRNNIAV 605
DB 574 IMHCI--IKRN--MNLVAVITPEKENSINI 601
RESULT 11
ID Q5JZY7_9BACL PRELIMINARY; PRT; 785 AA.
AC Q5JZY7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DE 21-FEB-2006, entry version 7.
ID IspB protein.
OC Brevibacillus laterosporus.
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
OX NCBI_Taxid=1465;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1629973; DOI=10.1016/j.gene.2005.07.033;
RX Mestrovic N., Rading O., Abad P., Plohl M., Castagnone-Sereno P.;
RT "Conserved and variable domains in satellite DNAs of mitotic
parthenogenetic root-knot nematode species";
RL Gene 362:44-50(2005).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RU Van Rie J.;
RA Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AJ872073; CA143278.1; -; Genomic DNA.
DR GO; GO:0005576; Cytoplasmic region; IEA.
DR GO; GO:0009405; P; pathogenesis; IEA.
DR InterPro; IPR003896; Anthrax toxinB.
DR InterPro; IPR011658; PA14.
DR InterPro; IPR013145; PA14 rel.
DR Pfam; PR03495; Binary toxB; 1.
DR PRINTS; PR01391; BINARYTOXB.
SQ SEQUENCE 785 AA; 87619 MW; F8A87A37D91A4D1E CRC64;
Query Match 20.8%; Score 786; DB 2; Length 785;
Best local Similarity 30.7%; Pred. No. 1.1e-29;
Matches 236; Conservative 119; Mismatches 299; Indels 114; Gaps 27;
QY 4 KOENRLNSES--SSQGLIGYFSDLNFAQPMVYTSSTTGDLSIPSSLENIIPSENGYF 62
DB 42 QENQ---EKVDKRGKLGIGYFSGKEFNHLLTLPAPTNDTLIYDQTVDFLDKQOQYOS 98
QY 63 AIWSGFIKYKSDYTPATSDNHYTMVDQVINKASNSKIKLEKRLVQIKI 122
DB 99 IRMIGLIQSEKTEGDFPNLSDDKMAIEIDKTIHSKGNKQVHLEKGLVPIKLEYOS 158
QY 123 ENPTEKSG---LDPKLYWTDSONKKEVISDNLOPELKOKSNSRKRKSTASAG----- 172
DB 159 DOIUNDSKIFKEFKLYKVDQSQSHQVOLDRLKRPFKKKTQQLERAKSTNITQNM 218
QY 173 ---PTVPDRNDNGIPDSLEVEGYTDV--VKNKRTFLSPWISNIHEKKGLTRYKSPK 225
DB 219 KRDEBATDTDQGISIPDMEENGTYTQNKVAVKMDSEFA-----KGYTFVSNPFD 269
QY 226 WSTASDPYDFEKTGRIDKNVSPKARHPLVAAPYIVHYDMENIISKNEDOSNTDQ 285
DB 270 SHTVGDPYDYDKAARDLILANAKETFNPLVAAPSVNVLKRVILSPNEDIS----- 322
QY 286 TTTISKNTSRD--ANTVGVISAGVNGPTGNI--TTSAGFSNSSTVAIDHSI 342
DB 323 -NSVSHSSTNWSYNTTEGASIEAG-----SGPLGISVSVSNAYQSEVA----- 367
QY 343 ERTMAETM-----LNTADTARLANIRYVNTGTAPYVNLPTTSLVIGKNOGLATTIKAK 398
DB 368 -KEMGTSTGNTSQFNTASAGYLANAVRYNNGTGALYEVKEFTTGFL--DNDYVATITAKS 425
QY 399 NQLSQTLPANNYPKSNLAPIALNADDFSTPTMTNNOFLEKTKQLRLDTPQYGN 458
DB 426 NSTALISPSGESYPKKGQNGIAINTMDDFNSHPITLTKQOLQIFNNKELMETNQADG- 484
QY 459 IATYVNEGRVAVDNGSNSEVLPOIQTARTI--FNGKDLNVERRIAANVPSDPLET 518
DB 485 --VYKIKDTSNGNIVTGGENNGVYIQOQATYASIIYDTGS--GVSEKVAKNDVNDPKDT- 540
QY 519 PMMTLKALKIAF--GFNEPNGNLQYQKQDITEPDR--NPDQOTSQNIKNOLELNATN--T 572
DB 541 PSLSLKALKGYPEIKERKQGLIYNDKPIYESSWMTYLDENTIAKEVGEQNDIDGKPK 600
QY 573 NIYTVLDKIKLANAKNILLRDKRFHYD-----RNINAVGADSSVKEAREVYINSSTEG 627
DB 601 DVKQLFD--VKLTPKKNFTIKLATL--YDGAEDSSPTDVGISPLGEMAFKPPINNVEGGA 658
QY 628 LNIIDKDIRKILSGYVLEIDTGLKEVINRYDMNLSLQDQKTFIDFKKYNKLP 687
DB 659 TGRKQYQSLSKNDGY-----YGMALSS-----EVSNSKL----- 688
QY 688 YLSNPYKNNVAVYKENTINPSEN--GDTSTNGI--KKILIFSKKGYE 733
DB 689 ---KKNYQYIISMSTKADAGVEPTVYVMDNLNGIYDKKLGKLSNGYQ 733

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RESULT 12
O5JZ26_9BACL PRELIMINARY; PRT; 871 AA.
ID O5JZ26_9BACL
AC O5JZ26_9BACL
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DR Brevibacillus laterosporus.
DR Iapla protein.
OS Brevibacillus laterosporus.
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
CC NCBI_TaxID=1465;
RN [1]
RX NUCLEOTIDE SEQUENCE.
RX PubMed=16229973; DOI=10.1016/j.gene.2005.07.033;
RA Mestrovic N., Randig O., Abad P., Pichl M., Castagnone-Sereno P.;
RT "Conserved and variable domains in satellite DNAs of mitotic
RT pathogenetic root-knot nematode species.";
RL Gene 362:44-50(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RP Van Rie J.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
CC EMBL; AJ871923; CAI40767.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR003896; Anthrax_toxinB.
DR InterPro; IPR01658; PA14.
DR InterPro; IPR013145; PA14_rel.
DR Pfam; PF03495; Binary_toxB.
DR Pfam; PF07691; PA14_1.
DR PRINTS; PRO1391; BINARYTOXINB.
DR SEQUENCE 871 AA; 97391 MW; 82P5EAA16763FDC5 CRC64;

Query Match 20.6%; Score 776; DB 2; Length 871;
Best Local Similarity 31.5%; Pred. No. 3.7e-29;
Matches 237; Conservative 123; Mismatches 296; Indels 96; Gaps 32;

OY 11 ESESSOGLGYFSDNLFQAPMVVTSSTGDLSPSELEN--IPSENQYQSAIMNGF 68
DB 47 DNQIDREGILGYFFGKDFN-DLTFAPRDTLTYDQATATLVQKHQETHSIRWIGL 105
OY 69 IKVKSDEYTFATSDNHNVTMMVDDQEVINKASNSNKIRLEKGRLYQIKIYQYR----- 122
DB 106 IQSSATGDFTFGLSDENALIELDKVISEKNNQSVHLEKGLVQIKIEYQSDALHI 165
OY 123 ENPTEKGLDFKLYWTDSONKKEVISSDNLQLPELKOKSSNRKKSSTAG----- 172
DB 166 DNKIFK--ELKLFKIDSQNHSGOVQODELRNPEPKKEQVFLKKAASKNLTFTQTKEDI 223
OY 173 PTVPRDNDGIFDSLEVBGYTVDVGNKRTPLSPNHSNHEKKGGLTKYSSPEKMTADP 232
DB 224 DEDTDTDGDSPDWVEENGTY--IQNK--VAVKWDLSL-ASKGYOKFTSNPLAHTVGP 278
OY 223 YSDFEKTGRIIDKNYSPEARHPLVAAYPIVHDMENIILSKEDQSTQNTDQRTISKN 292
DB 279 YSDYKARADMELSNAKETPNPLVAAPSVNLSLEKVLISKEDSHSVESQ-----STN 334
OY 293 TSTSHDANTGVVISAGYONGFTGNITTSAGFSNSNSTVALDHSLSLAGEFTMAETWG- 351
DB 335 WSYT---NTEGVNVAAGW-----SGLGSPFGVSVNQHSETVANEMGSAINDGT 380
OY 352 -LNTADTARLNATNYVNTGTAIPYNVLPFTSYLQKQTLATITAKENQSLIAPNNY 410
DB 361 HINGBSAIVLNNAVRYNNVGTALVETKRTJTFIL-DGTTIGITAKETVATLTLLPDQS 439
OY 411 YPSKMLAPIALNAODFSSTPTTMVNGP-LLEKTKQLRLDTPDQVGNIAATYENGAV 469

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DB 440 YPEKGNKGIANTWDDFNSRPIPLNKEQLNTYLSNKKPILLETDOVSGKVAIKD-TNGNI 498
OY 470 RVDTSNWSSEVLPOIQETTAIIF-NGKDLNLYERRIAAVNPSDELTTKDMTLKEALK 528
DB 499 TI--AGDWNGITDEISAKTASIIYDNGNQMS--EKRYAAKQYTNBEDKT-PNLSYKEALK 553
OY 529 IAF--GFEPEPKNQYOOGKDIITEFDNF--FPQOTSNIKNQALAEINAT-----NIYTVLD 579
DB 554 LAYDEIEKKGGLFYNDQPIFEASVQSYVDYETAKQIRKQLDNSTGSFKQVKNLYDV-- 611
OY 580 KIKLNKKNILIRDKRFHYD--RNNTAVGADSESVKAEHREYVNSTEGILLINDKIR 636
DB 612 --KLEPKNFTIKTSTL-YDGESEDNTKIG-----NMYYTYVYVNGNTG-----KKQYR 657
OY 637 KILSGYVEI--EETEGKXYINDRYDMLNITSLRQDKTFIDPKVNDKLPVYSNPN- 693
DB 658 SANRGAFTLESTESKKNKLNKI-DYVSL--YMKADSKSVDIIEIDKQSIYTDNITL 713
OY 694 -----YKVNVAAYTKENTINP-SENGDSTN 719
DB 714 DHVGQRINILVPLBEGNEINTTISIKDGGQTN 745

RESULT 13
O844J8_BACTU PRELIMINARY; PRT; 775 AA.
ID O844J8_BACTU
AC O844J8_BACTU
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE ViplAC.
GN Name=ViplAC;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15357725; DOI=10.1111/j.1365-2672.2004.02365.x;
RA Shi Y., Xu W., Yuan M., Tang M., Chen J., Pang Y.;
RT "Expression of vip1/vip2 genes in Bacillus thuringiensis and the analysis of their signal peptides.";
RL J. Appl. Microbiol. 97:757-765(2004).
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CC -----
CC EMBL; AY245547; AAO86514.1; -; Genomic DNA.
DR HSSP; P13423; IACC.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR003896; Anthrax_toxinB.
DR InterPro; IPR01658; PA14.
DR InterPro; IPR013145; PA14_rel.
DR Pfam; PF03495; Binary_toxB.
DR Pfam; PF07691; PA14_1.
DR PRINTS; PRO1391; BINARYTOXINB.
DR SEQUENCE 775 AA; 87111 MW; 416B25394361B731 CRC64;

Query Match 19.8%; Score 746; DB 2; Length 775;
Best Local Similarity 30.2%; Pred. No. 9e-28;
Matches 232; Conservative 128; Mismatches 292; Indels 116; Gaps 32;

OY 4 QENRLNSESSESGGLGYFSDNLFQAPMVVTSSTGDLSPSELEN--IPSENQYQ 61
DB 42 QKNQ---QKENDRKGILGYFFGKDF-SNLTMPFAPTRDNTLTYDQATANKLIDKKQDQYQ 97
OY 62 SAWSGFLIKVKSDEYTFATSDNHNVTMMVDDQEVINKASNSNKIRLEKGRLYQIKIYQ 121
DB 98 SIRWIGLQSKRGKDFYNNLSDEDAIIEIDKILSNKGRKQVNHLEKGLVPIKIRYQ 157
OY 122 RENPTEKGLD-----PFLYWTDSONKKEVISSDNLQLPELKOKSSN----- 162

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DB 158 SD--TKFNIDSKTPEKFKLTKIDQSQOQVKBDELBNPEFNKESREFLAKASKTNFEM 215
QY 163 SRKKSTSGAPTPPDNDGIPDLSLEVETTVDKKRTFLSPWISNIHEKKGLTKYKS 222
DB 216 QKKRDRIDBD---TDYDGDSDIPDLMEENGYT--IQNK--VAVWK-DDKFAQOQGVYVYLS 267
QY 223 PEKMSFASPDSPDFEKTVRIDKNGVPEARHPVAAYPIVHVMMENITISKNDQSTQNT 282
DB 268 PYOAHVTGDPYDWTWKAAGDIPFSNAATNPVLAAPSPSINVMRKMTISKD-----SNL 322
QY 283 DSQRTISKNTSTSRDANTVGSISAGY-ONGFTGNITTSAGPSNSSTVAIDHSLSLA 341
DB 323 SNSBAHSNNSYTY--ANSBGASIEAGFGKFSFGV--SANT--QHTETVGS----- 370
QY 342 GERTW---AETWGLNTADTARLANIRVYNTGTAPVYNTLPTTSVLVGNQTLATTKAK 397
DB 371 ---WQNSKSNTEQFNSASAGYANAVHYNVGTGIGYDAQPTTSPIL-QDSTIATITAK 425
QY 398 ENQLSQIILPNVYPSKLNAPILANQDDSSPTPTMNNQPLEKTKQLRLDTDOVYG 457
DB 426 SNATLSTISGDRYPASK-EGISLKTMDDPNSHPITLNFQDLADVANNVEYKINTQDTG 484
QY 458 NIATVFNKGRVAVDGSNMSEVLPOIETTARIIIFNGKDLNVERRIAANPSDELETT 517
DB 485 RYGIIGVDG---KAEIGDRKSPITIDIKGRTASIIIDPADGKALFTRIAKOVKNEDKT 541
QY 518 KQDWTIKKALIKAFG---FNEPENGLOYOQGD---ITFEDF-----FDQOTSQNTK 563
DB 542 -PSLTIKEGKLIAVPSISSEDKOGLIFEYKNDGKVTYKQSLSEENIMPLDSDTSKEFE 600
QY 564 NQLAELANNTIYVLDKIKLANAKNILLIDKRFHYDRNNAVAGADESVYKAREVINS 623
DB 601 ROLSDSGSAGLV---DILKTPPMTTIR-----LATVQLDFDQFSAYPWNATWSD 649
QY 624 TEGSLT-----LNIIDKDIRK-----ILSGYIVB--IEDTEGLKEVI---NDRYD 661
DB 650 KFGNLALGSLATPQESKTIIPKDKAPNDYILTGIIKHDFTTDSLSGLVATTKDNFE 709
QY 662 MNISLSRODKTIFDKKXNDKLPYISNPNKYVAVYATKENTIN 709
DB 710 MNMGTSIFSQNSGSGFKFTIKTQ-NISG-DYILDSIQMKKNNDVN 755
RESULT 14
Y6163_BACAN STANDARD; PRT; 225 AA.
ID Y6163_BACAN STANDARD; PRT; 225 AA.
AD P13422; O8KXK2; O9X377;
DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 3.
DT 07-MAR-2006, entry version 39.
DE Hypothetical protein PXOI-111/BXA0163/GBAA_PXOI_0163.
GN OrderedocusNames=PXOI-111, BXA0163, GBAA_PXOI_0163;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89172073; PubMed=3148491; DOI=10.1016/0378-1119(88)90439-8;
RA Welkos S.L., Lowe J.R., Eden-McCutchan F., Vockin M., Leppla S.H.,
Schmidt J.J.,
RT "Sequence and analysis of the DNA encoding protective antigen of
Bacillus anthracis."
RL Gene 69:287-300(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=sterne;
RC MEDLINE=9945463; PubMed=10515943;
RA Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,
Martinez Y., Rieke D., Svensson R., Jackson P.J.,
RT "Sequence and organization of pxoi, the large Bacillus anthracis

RT plasmid harboring the anthrax toxin genes.";
RL J. Bacteriol. 181:6509-6515(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ames / isolate Florida / A2012;
RX MEDLINE=22061436; PubMed=12004073; DOI=10.1126/science.1071837;
RA Read T.D., Salzberg S.L., Pop M., Shumway M., Unayam L., Jiang L.,
Holtapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.,
RT "Comparative genome sequencing for discovery of novel polymorphisms in
Bacillus anthracis."
RL Science 296:2028-2033(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ames ancestor;
RA Ravel J., Rasbo D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
Walson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.,
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC CC
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CC Distributed under the Creative Commons Attribution-NonDerivs license

CC EMBL, W22589; AAA22636.1; ALT_INIT; Genomic DNA.
DR EMBL, AF065404; AAD32415.1; ALT_INIT; Genomic DNA.
DR EMBL, AB011190; AAM26108.1; -; Genomic DNA.
DR EMBL, AB017336; AAT28903.2; -; Genomic DNA.
DR PIR, G59104; G59104.
DR PIR, I39933; I39933.
DR HSSP, P13423; IACC.
DR GenomeReviews; AE017336; GR; GBAA_PXOI_0163.
DR TIGR, GBAA_PXOI_0163; -.
DR InterPro; IPR003896; Anthrax toxinB.
DR Pfam; PF03495; Binary toxinB; 1.
KW Complete proteome; Hypothetical protein; Membrane; Plasmid;
KW Transmembrane.
KW CHAIN 1 225
FT FT
FT FT
FT TRANSMEM 181 203
FT CONFLICT 114 114
FT CONFLICT 205 225
FT FT
SQ SEQUENCE 225 AA; 25402 MW; 2E121B854295F9C8 CRC64;
Query Match 7.9%; Score 296.5; DB 1; Length 225;
Best Local Similarity 37.2%; Pred. No. 9.7e-07;
Matches 68; Conservative 38; Mismatches 54; Indels 23; Gaps 6;
QY 566 LAELNANTNITYVLDKIKLANAKNILLIRDRPHYDRNNAVAGADESVYKAREVINSSTE 625
DB 1 MESLGIINNINMLDRKLNAAKNIIIVRP-YHYDNGNIVGVDDSYLNAKAYQILMWSSD 59
QY 626 GLILNIDKDIRKILSGYIIEDETE-----GIKEVINDRYMLNITSSLRDGS 672
DB 60 GVSINLDEVDNQALSGYMLQIKKPSNHLTNSPVYITLAKDGSVGLHYVLS-----DG 113
QY 673 KNPIDKKKNDKLPYISNPNKYVAVYATKEN-TIINSENGDSTNGKILIFSKGS 731
DB 114 TGFIDPNKFDENWRSLV-DPGDDVYVAYKDFNAVTRDENGINA-NKLKNTLVLSGKI 171
QY 732 YEI 734
DB 172 KEI 174
RESULT 15
ID 06FNZ8_CANGA PRELIMINARY; PRT; 1305 AA.
AC 06FNZ8;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.

19-JUN-2004, sequence version 1.
 DT 21-FEB-2006, entry version 20.
 DE Similar to sp|P12753 Saccharomyces cerevisiae YNL250w RAD50 DNA repair
 DE protein.
 OS OrderedLocustNames=CAGL007788g;
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 CC NCBI_TaxID=5478;
 CC [1]
 NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 2001 / CBS 138;
 RC PubMed=15229592; DOI=10.1038/nature02579;
 RA Lafontaine I., de Montigny J., Marc C., Nevegliese C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anichoud V., Babour A., Barde V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne B., Bleykasten C.,
 RA Boissarie A., Boyer J., Catolico L., Confanieri F., de Daruvar A.,
 RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreay F., Hemeguin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.-M., Nikolaki M., Ozas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
 RA Zenou-Meyer M., Zivanovic Y., Bojotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.,
 RL "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
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EMBL: CR380956; CAG6097.1; -; Genomic DNA.
 DR GO: GO:0005694; C:chromosome; IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0030870; C:Mei1 complex; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016887; F:ATPase activity; IEA.
 DR GO: GO:0004518; F:nuclease activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0051276; P:chromosome organization and biogenesis; IEA.
 DR GO: GO:0006281; P:DNA repair; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR003439; ABC transp_like.
 DR InterPro: IPR004584; Rad50.
 DR InterPro: IPR007517; Rad50_Zn_hook.
 DR InterPro: IPR003395; SMC_N.
 DR InterPro: IPR013134; Zn_hook_Rad50.
 DR Pfam: PF04423; Rad50_zn_hook; 1.
 DR Pfam: PF02463; SMC_N_1.
 DR TIGRFAMs: TIGR00606; rad50; 1.
 DR Complete proteome.
 SQ SEQUENCE 1305 AA; 15066 MW; 7489860D317CEFA0 CRC64;

Query Match 6.2%; Score 232.5; DB 2; Length 1305;
 Best Local Similarity 20.5%; Pred. No. 0.012; Indels 279; Gaps 39;
 Matches 175; Conservative 135; Mismatches 264;

1 EVKQENRLIN-----ESSSSQGLGYPFSDLNFPAPVVTSTTGLSIPSSR 49
 DB KYKQINBKINDVQSDVDVEQELSESINGSLDLPFSKNQNFQSVLRIFETIANSTISAATQ 284
 QY 50 LENTDS-----EN--QYFQSAIWSGFIVYKKSDEYTPAITSADNHTVMVDDOE 95
 DB 285 IERLNSISIEKLDMPKYDLENILKNFSESIEQKELDVKRLESKIAS-----DRQK 333
 QY 96 VINKASNSNKIRLREKGRLYQIKIYQYR-----ENPTEKGLDFK 133
 DB 334 LENCQKQSRRLMLQGGELPAKGLQNTKTSFQDTIRQIKDEHKLDLNAEPPQRRVDHT 393
 QY 134 LYWTDSQNKKEVYISSDNLQLPKLKQKSSNSRKRRSTSGAPTVPRDRNDGIPDLSLEVEG-- 191

DB 394 L-----KKKADMESSVNEAISKLEETKQNLK-----SDSIRNSINLEBQK 435
 QY 192 ---YTVDYK-----NKRTFLSPWISINHEKGLITKYSPEKMSSTAPDYSPEKVTG 241
 DB 436 LSYIESDILKQATLDDQKQIISI PADIEE-----QKAKKAVMSKLSKELQEPK--- 487
 QY 242 RIDKNSPEARHPIVAAYPIVHVDMENIILSKNDS-----TQNTDSQRTTISKNTSTS 296
 DB 488 --ENNIT-----DINNQIKSNBELSKSELQAQIETDLQNYSKSKSLTS 529
 QY 297 KDANTGVGISAGYQNGFTGNTTSAGFSNNSSTVAIDHSLAG-RTAETMTGLATA 355
 DB 530 TKLSVL-IENNDEKQNB-I-NKITTALINDTMIXEMGLDVKQLSFEKTHYIALQNKIA 586
 QY 356 DTALNNIRVYNGTAPIYVNVLPPTSILVGLKNOT-----LATIKAKENQLSQ-----IL 405
 DB 587 -----TKLKAFN-----ISKSTBLEYELANTCKGKVNLIQHKKEKIL 625
 QY 406 APNNYPS-----KNLAPIALNAODDFST-----PTVMYNOFLBLEKTQRLDTDQ 454
 DB 626 NINSVLPEDCSIEDYDVLLETETVSYKTALENLKHGHQTTLEFNR-----KALBVAINDC 680
 QY 455 VYGNIAIYVNFENGKVRVDTSNMSEVLPOIQETTRARIIENGKDLNLYERRIAAVNPSPPL 514
 DB 681 CY--LCRSRFENTTEFR-----SKILKEKKEKT-----DKFEB-----SL 713
 QY 515 ETTKPDMLKEALKIANGFENPNGLQYQKDIETEPDFENPDQOTSQ----- 560
 DB 714 KTTLEDE--KEYL-----NNLRALAEKDI-----YNLSISSESALODRISQLSKE 757
 QY 561 --NIKQOLAEILNATNITYVLDKIKLNAKMNIILDKRFHYDRNNIANGADE----- 609
 DB 758 LDNKKSEVAEAN-----TTIEKTK-----EKRDHCD-NYIKPMKDIDYLQKEIY 801
 QY 610 --SVKKAHREYVINSSTEG-----LLANIDKQIRKILSGIYIEIETBGLKAVINDRY 660
 DB 802 NHEEKSKINDVIRISSAENGDSVTMBQLODNQKSTRELIWKIRSEIBELQORENITSKN 861
 QY 661 DMLNLSLRQ-----DGKTFIDPKKYNDKL---PLYISNPYKVVAVYTKEN 705
 DB 862 NTL-INQIRQANDVVAETIEKQFDMKVTIIQEOIANDKHAIBELTNSKESIKLHINDLSKV 920
 QY 706 TIINPSNGDTST 718
 DB 921 EMLKNSEKIST 933

Search completed: August 11, 2006, 20:26:06
 Job time : 315 secs